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(54) **DIMERIC DIAGNOSTIC ARRAYS**

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C07H 21/04	(2006.01)

(52) **U.S. Cl.**

CPC C12Q 1/6837 (2013.01); C12Q 1/689 (2013.01); C12Q 1/6895 (2013.01)

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435/287.2; 436/94, 501; 536/23.1, 24.3,
536/24.33

See application file for complete search history.

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(57) **ABSTRACT**

The invention provides dimeric diagnostic arrays and methods for their use.

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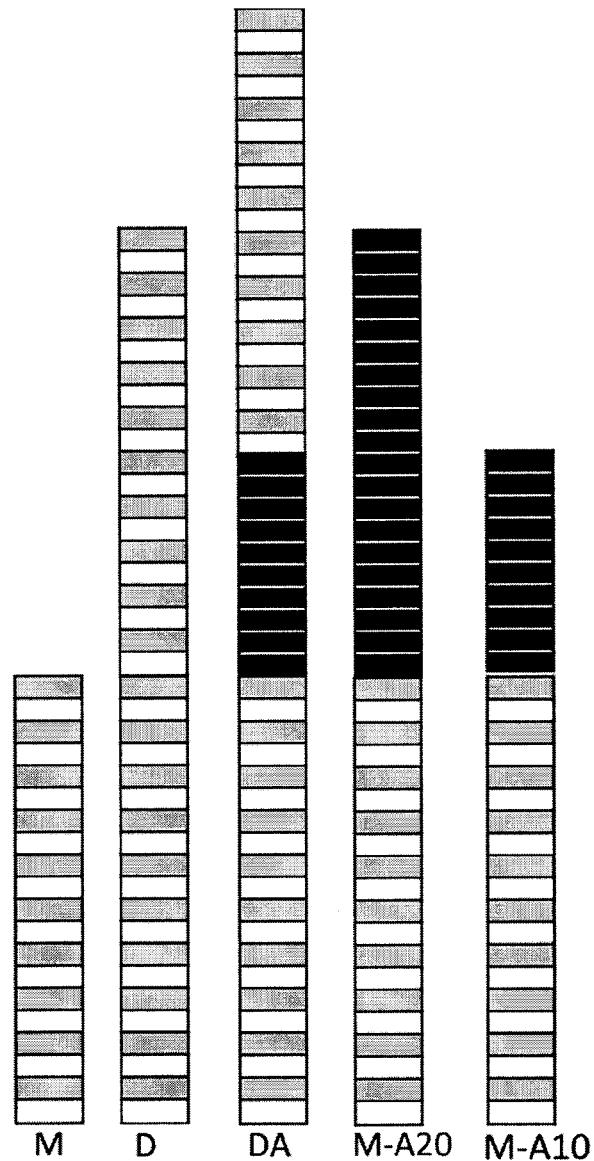


Fig. 1

	1	2	3	4	5	6	7	8	
A	ITS4R.A	Pa1RA	Pa2RA	Pa3RA	ITS221A	Fs4RA	Fs6RA	Fs13RA	DA
B	ITS4R	Pa1R	Pa2R	Pa3R	ITS221R	Fs4R	Fs6R	Fs13R	D
C	ITS4	Pa1	Pa2	Pa3	ITS221	Fs4	Fs6	Fs13	M
D	ITS4A10	Pa1A10	Pa2A10	Pa3A10	ITS221A10	Fs4A10	Fs6A10	Fs13A10	M-A10
E	ITS4A20	Pa1A20	Pa2A20	Pa3A20	ITS221A20	Fs4A20	Fs6A20	Fs13A20	M-A20
F	ITS2R.A	Rs1RA	Rs2RA	Rs3RA		Fo1RA	Fo2RA	ITS2	M
G	ITS2R	Rs1R	Rs2R	Rs3R		Fo1R	Fo2R	ITS2A10	M-A10
H	ITS2	Rs1	Rs2	Rs3		Fo1	Fo2	ITS2A20	M-A20

	1	2	3	4	5	6	7	8	
A	Pa				Fs				B
B									
C									
D									
E									
F									
G									
H									
	Rs				Fo				

	1	2	3	4	5	6	7	8	
A	Pa				Fs				C
B									DA
C									D
D									M
E									M-A10
F									M-A20
G									M
H									M-A10
	Rs				Fo				M-A20

	1	2	3	4	5	6	7	8	
A	Pa				Fs				D
B									M
C									M-A10
D									M-A20
E									M
F									M-A10
G									M-A20
H									M
	Rs				Fo				M-A10

	1	2	3	4	5	6	7	8	
A	Pa				Fs				E
B									DA
C									D
D									M
E									M-A10
F									M-A20
G									M
H									M-A10
	Rs				Fo				M-A20

Fig. 2

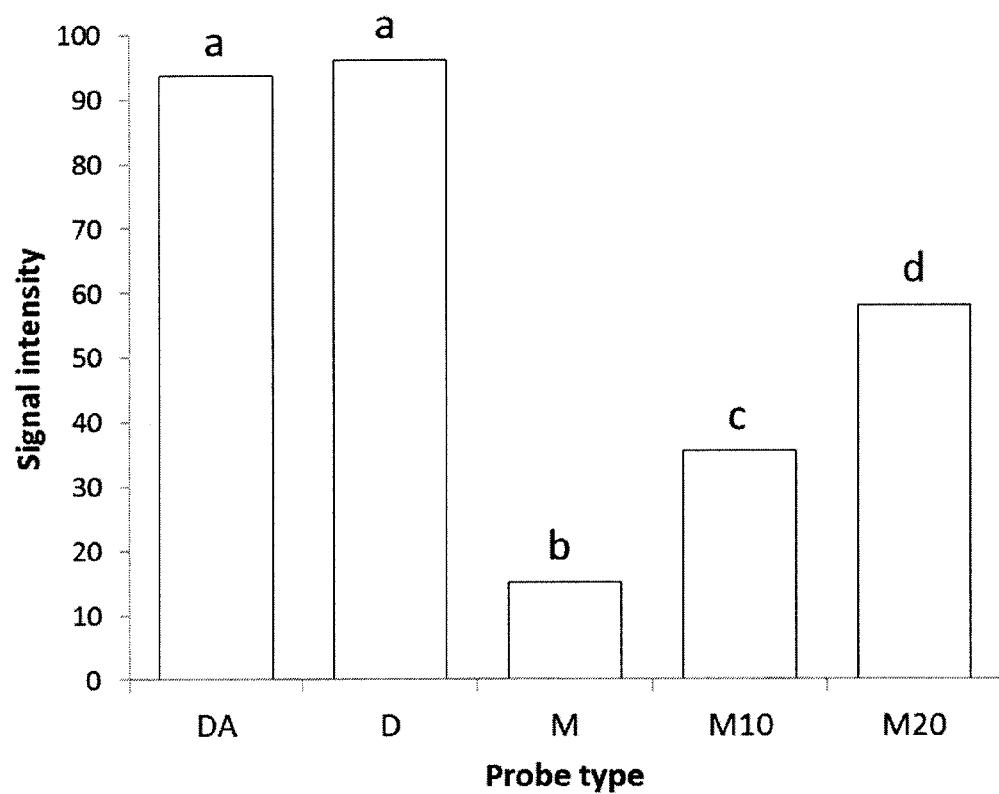


Fig. 3

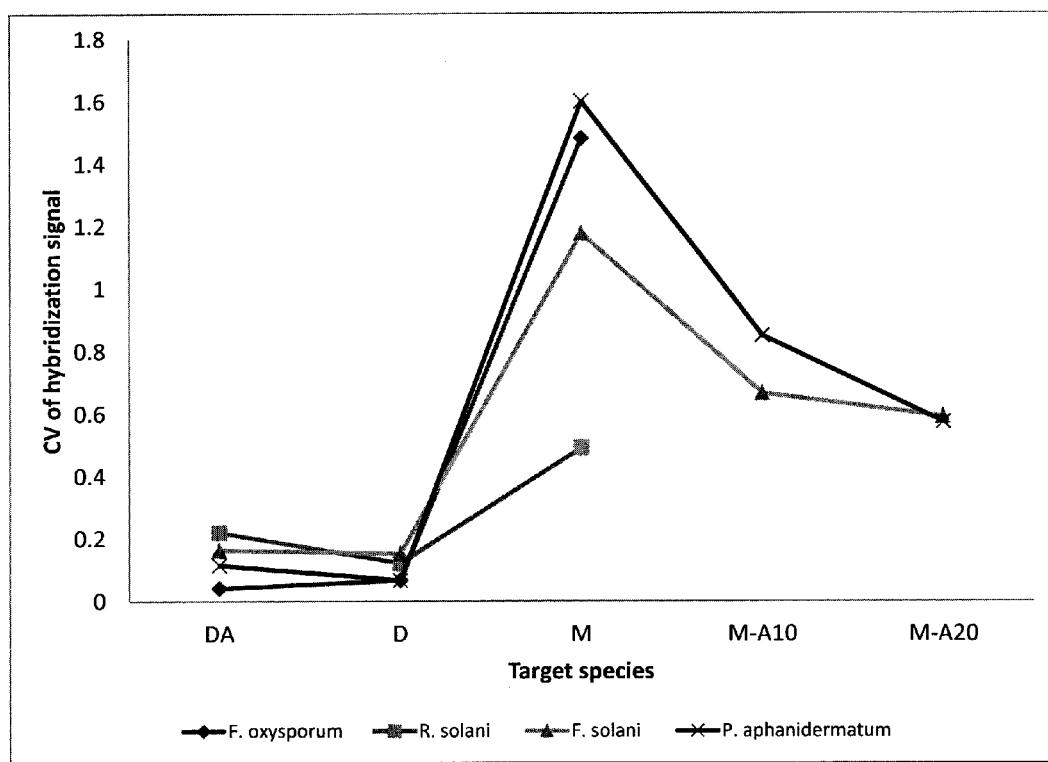


Fig. 4

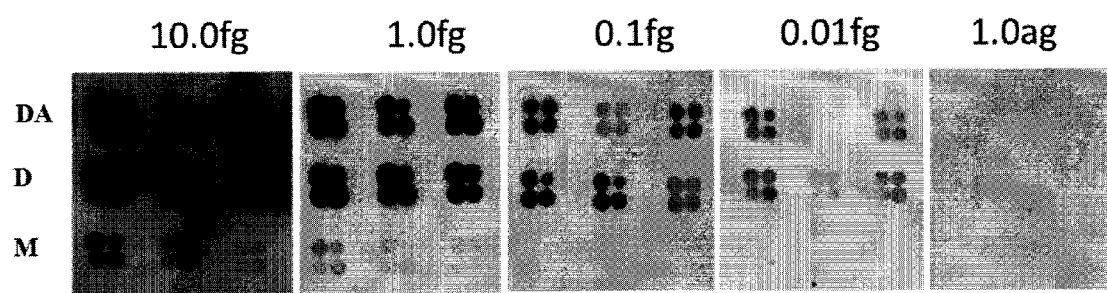


Fig. 5

1**DIMERIC DIAGNOSTIC ARRAYS****RELATED APPLICATION(S)**

This application claims the benefit of priority of U.S. Provisional Application Ser. No. 61/476,143 filed on Apr. 15, 2011, which application is herein incorporated by reference.

Sequence Listing

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Sep. 4, 2012, is named 08035006.txt and is 68,827 bytes in size.

BACKGROUND

Detection and identification of pathogens, e.g., microbial plant pathogens, poses a challenge because different pathogens may infect the same host concurrently and may produce similar symptoms. In the absence of clear distinctive symptoms and signs, plant disease diagnosticians may use the host identity, time of the year and prevailing weather conditions to associate the pathogen with the disease. Accurate pathogen identification is the first step in disease management. Misidentification of a pathogen may lead to poor disease control, crop damage and ultimately reduced yield. There is therefore a need for improved disease surveillance, more rapid diagnoses, and accurate remedial measures in the shortest time possible.

SUMMARY OF CERTAIN EMBODIMENTS OF THE INVENTION

Certain embodiments of the present invention provide an array that comprises a first plurality of dimeric probes that hybridize to a first target nucleic acid sequence, wherein the dimeric probes each comprise a first hybridizing nucleic acid sequence and a second hybridizing nucleic acid sequence linked together, wherein the first and second hybridizing nucleic acid sequences are the same and hybridize to the first target nucleic acid sequence. In certain embodiments, the dimeric probe comprises a third hybridizing nucleic acid sequence that hybridizes to the first target nucleic acid sequence and is the same as the first and second hybridizing nucleic acid sequences.

Redundancy in the array may improve accuracy and analytical power through over-representation. As used herein, the phrase a "plurality of dimeric probes" means at least two (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10) probes that hybridize to the same target nucleic acid sequence.

In certain embodiments, the first plurality of dimeric probes comprises at least two (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10) probes.

In certain embodiments, the first and second hybridizing nucleic acid sequences are linked directly together.

In certain embodiments, the first and second hybridizing nucleic acid sequences are linked together via a nucleic acid linker sequence.

In certain embodiments, the nucleic acid linker sequence is a polyadenine linker (e.g., about 5-15, e.g., about 10 nucleotides in length).

In certain embodiments, the dimeric probes are about 40-60 nucleotide in length.

In certain embodiments, the dimeric probes are about 40-48 nucleotide in length.

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In certain embodiments, the dimeric probes are about 50-58 nucleotide in length.

In certain embodiments, the array comprises a second plurality of dimeric probes that hybridize to a second target nucleic acid sequence.

In certain embodiments, the second plurality of dimeric probes comprises at least two (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10) probes.

As redundancy may improve the accuracy and analytical power of the array, probes that recognize different target nucleic acid sequences in the same pathogen may be used.

Accordingly, in certain embodiments, the first and second pluralities of probes hybridize to target nucleic acid sequences in the same pathogen.

15 The array may also be designed to detect more than one type of pathogen. DNA sequences available in publicly accessible databases (e.g., GenBank) allow for the creation of signature probes specific to a species or infra-species target. Accordingly, one skilled in the art may design a dimeric probe 20 as described herein, which is specific to any given species or sub-species, wherein the genomic sequence of the species or sub-species is known (e.g., full or partial), using techniques known in the art or described herein (e.g., Example 1 or 2).

Accordingly, in certain embodiments, the first and second 25 pluralities of probes hybridize to target nucleic acid sequences in different pathogens.

In certain embodiments, the array comprises more than two pluralities of dimeric probes (e.g., 3-6) that hybridize to different target nucleic acid sequences.

30 In certain embodiments, each plurality of dimeric probes comprises at least two (e.g., 3, 4, 5, 6, 7, 8, 9, 10) probes.

In certain embodiments, the pluralities of probes hybridize to target nucleic acid sequences in the same pathogen.

In certain embodiments, the pluralities of probes hybridize 35 to target nucleic acid sequences in different pathogens.

In certain embodiments, the array comprises pluralities of dimeric probes that specifically hybridize to target nucleic acid sequences in about two (e.g., about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33 or 34) different pathogens (e.g., each plurality of dimeric probes hybridizes to a specific target sequence and each target sequence is particular to a given pathogen). In certain embodiments, the array comprises pluralities of dimeric probes that specifically hybridize to target 45 nucleic acid sequences in about 35 different pathogens. In certain embodiments, the array comprises pluralities of dimeric probes that specifically hybridize to target nucleic acid sequences in about 50 different pathogens. In certain embodiments, the array comprises pluralities of dimeric probes that specifically hybridize to target nucleic acid sequences in about 75 different pathogens. In certain embodiments, the array comprises pluralities of dimeric probes that specifically hybridize to target nucleic acid sequences in about 100 (e.g., about 125, 150, 175, 200, 250, 300, 350, 400,

50 450, 500, 750, 1,000, 2,000, 3,000, 4,000, 5,000, 10,000, 25,000, 50,000, 75,000, 100,000, 500,000, etc.) different pathogens.

In certain embodiments, the target nucleic acid sequence is located in an internal transcribed spacer sequence of an rRNA gene. In certain, embodiments, the target nucleic acid sequence is located in EF1-alpha, Beta-tubulin, RPB1, SSU, or LSU.

In certain embodiments, the pluralities of dimeric probes are selected from the sequences listed in Table 2 or Table 7.

65 In certain embodiments, the pluralities of dimeric probes are selected from SEQ ID NO:4 to SEQ ID NO:9, SEQ ID NO:19 to SEQ ID NO:24, SEQ ID NO:28 to SEQ ID NO:33,

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SEQ ID NO:42 to SEQ ID NO:45, SEQ ID NO:48 to SEQ ID NO:51, SEQ ID NO:57, SEQ ID NO:58 and SEQ ID NO:73 to SEQ ID NO:301.

In certain embodiments, the pluralities of dimeric probes are selected from SEQ ID NO:4 to SEQ ID NO:6, SEQ ID NO:19 to SEQ ID NO:21, SEQ ID NO:28 to SEQ ID NO:30, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:57, and SEQ ID NO:73 to SEQ ID NO:301.

In certain embodiments, a target sequence is from a fungal, viral, or bacterial pathogen.

In certain embodiments, a target sequence is from a pathogen of turfgrass.

In certain embodiments, a target sequence is from *Brumaria graminis*, *Bipolaris zeicola*, *Colletotrichum cereal*, *Eudarluca caricis*, *Puccinia coronata*, *Puccinia persistens* var *triticia*, *Puccinia striiformis*, *Puccinia graminis*, *Puccinia graminis* f. sp. *Triticici*, *Pythium volutum*, *Pythium torulosum*, *Pythium arrhenomanes*, *Pythium deliense*, *Pythium rostratiformis*, *Pythium rostratum*, *Pythium aphanidermatum*, *Pythium myriotylum*, *Pythium arrhenomanes*, *Rhizoctonia solani*, *Ceratobasidium cereal*, *Waitea circinata*, *Rhizoctonia zeae*, *Waitea circinata* var. *circinata*, *Rhizoctonia oryzae*, *Sclerotinia homoeocarpa*, *Typhula incarnata*, *Typhula ishikariensis*, *Gaeumannomyces graminis*, *Magnaporthe grisea*, *Magnaporthe oryzae*, *Magnaporthe poae*, *Gaeumannomyces incrustans*, *Magnaporthe rhizophila*, *Magnaporthe salvinii*, *Microdochium bolleyi*, *Microdochium nivale*, *Gleocercospora sorghi*, *Laetisaria fuciformis*, *Lepidosphaeria korrae*, *Ophiopharella herpotricha*, *Ophiopharella agrostis*, *Limonomycetes roseipellis*, *Acidovorax avenae*, *Xanthomonas translucens* pv. *Poae*, *Curvularia trifolii*, *Trichoderma virens*, *Urocystis agropyri*, *Ustilago striiformis*, *Lycoperdon* spp., *Bovista*, *Agaricus*, *Marasmius*, *Lepiota*, *Athelia rolfsii*, *Gibberella zeae*, *Fusarium solani*, *Fusarium oxysporum* (*F. oxysporum*), *Fusarium* spp., *Poa annua* (RBCL), *Lolium perenne* (RBCL), *Agrostis stolonifera* (RBCL), *Poa annua* (matK), *Poa pratensis* (matK), *Agrostis stolonifera* (matK), *Motierella elongata*, *Fusarium equiseti* or *Waitea circinata* var. *zeae*.

In certain embodiments, a target sequence is from *Rhizoctonia solani*, *Pythium aphanidermatum*, *Fusarium solani* or *F. oxysporum*.

In certain embodiments, the array further comprises at least one positive control probe (e.g., a universal probe or a probe that hybridizes to a target sequence found in a class of pathogens, for example, such as a target sequence found in all fungi and/or oomycetes).

In certain embodiments, the at least one positive control probe is selected from SEQ ID NO:48 to SEQ ID NO:51 and SEQ ID NO:305 to SEQ ID NO:308.

In certain embodiments, the array further comprises at least one negative (i.e., internal) control probe (e.g., a probe that is designed not hybridize to any sequence from a target pathogen, such as, for example, a probe that contains nucleotide mismatches as compared to the positive control probe sequence, for example, two mismatched nucleotides).

In certain embodiments, the at least one negative control probe is selected from SEQ ID NO:57, SEQ ID NO:58, and SEQ ID NO:302 to SEQ ID NO:304.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Schematic representation of the five types of oligonucleotide probes used in the diagnostic macroarray. M=monomer (20-24 nt); D=dimer (40-48 nt); DA=dimer with polyadenine spacer (black boxes) of 10 bases between

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the two repeats (50-58 nt); M-A20=monomer with a polyadenine tail (black boxes) of 20 bases (40-44 nt); and M-A10=monomer with a polyadenine tail (black boxes) of 10 bases (30-34 nt).

FIG. 2. Macroarray design and hybridization results. FIG. 2A, Macroarray design. Specific probes for *Pythium aphanidermatum* (Pa), *Rhizoctonia solani* (Rs), *Fusarium solani* (Fs), and *F. oxysporum* (Fo, Fox) were spotted in the four shaded regions. Each of the five types of oligonucleotide probes was spotted in a row as follows: row A, DA; B, dimer; C, monomer; D, M-A10; E, M-A20; F (except F8 spotted with monomer), DA; G (except G8 spotted with M-A10), dimer; H (except H8 spotted with M-A20), monomer. Positive controls were spotted in A1, B1, C1, D1, E1, G1, H1, F8, G8, and H8. Internal controls were spotted in A5, B5, C5, D5 and E5. FIG. 2B, C, D and E show macroarray hybridization results with *P. aphanidermatum*, *F. solani*, *R. solani*, and *F. oxysporum*, respectively.

FIG. 3. Signal intensity comparison of different oligonucleotide probe types. Y-axis represents the mean signal intensity levels as measured with inverted grayscale values. For each probe type (X-axis), there are three independent probes targeting each species (four species tested) except for *F. oxysporum* which had two probes per probe type, making a total of 11 unique probes for M, D and DA oligonucleotide probe types. Only two species (6 unique probes) were tested for M-A10 and M-A20 probe types. Two isolates were tested for each species except for *F. oxysporum*, which had only one isolate available. The experiment was conducted twice. Means with the same letter do not differ significantly (Tukey test, P<0.05, n=11 for M, D, and DA whereas n=6 for M-A10 and M-A20).

FIG. 4. Coefficient of variation of hybridization signal intensity among different probe types for the four target species. The coefficient of variation (CV), is defined as the standard deviation divided by the means of the hybridization signals and is used here as a measure of the variation of signal intensity.

FIG. 5. Macroarray results when probes were hybridized with amplified *Rhizoctonia solani* from 10 \times serial diluted genomic DNA (10 fg to 1 ag).

DETAILED DESCRIPTION

Disease management can be improved with more rapid and more accurate pathogen detection and identification techniques. As described herein, a macroarray diagnostic technique with enhanced detection sensitivity has been developed. The use of repeat sequence probes (dimers) greatly improves the sensitivity of the macroarray. The dimeric probes reliably detected 0.01 fg target genomic DNA, which is lower than the detection limits of most currently available molecular diagnostic methods, such as the conventional PCR and real-time PCR. Dimer probes also had lower signal variability, thereby increasing the macroarray signal uniformity. This technique is useful for early human, animal or plant disease diagnosis, e.g., when only trace amounts of target microbes are present in a sample. The technique can be adapted and applied to microbial ecological studies and other research areas.

Traditionally, plant diagnosticians use direct observations and/or culturing of pathogens from diseased plant samples to make a diagnosis. These methods are often time consuming and insufficient to identify pathogens to the species level. More recent advancements, such as serology and PCR assays, also have their drawbacks. For instance, immunoassay typing with antibodies has been found to be less specific than DNA-

based methods. Quantitative PCR (qPCR), a widely used technology in medical, agriculture, and the food industry, offers an alternative detection platform. However, it is limited in terms of throughput where only one or a few pathogens can be detected in a test reaction (van Doorn et al., *Appl. Environ. Microbiol.*, 75, 4185-4193 (2009); Ivnitski et al., *Biotechniques* 35, 862-869 (2003); Uttamchandani et al., *Trends Biotechnol.* 27, 53-61 (2009); Lievens et al., *FEMS Microbiol. Lett.* 223, 113-122 (2003); Lievens et al., *Environ. Microbiol.* 7, 1698-1710 (2005)). Considering the vast diversity of pathogens, an ideal pathogen detection tool would be characterized by its monitoring capacity for a wide range of pathogen groups as well as by its accuracy and sensitivity (Lee et al., *J. Microbiol. Meth.* 65, 453-467 (2010)).

DNA diagnostic arrays are another molecular tool that offer a fast, culture-independent alternative for the detection of microbes from field samples (Lievens et al., *Phytopathology* 95, 1374-1380 (2005); Lievens et al., *J. Microbiol. Meth.* 80, 76-85; (2010); Zhang et al., *Plant Dis.* 92, 953-960 (2008); Gilbert et al., *J. Cotton Science* 12, 165-170 (2008)). The advantage of the array technique is its high throughput compared to other detection methods. Hundreds of different pathogens can be simultaneously detected with one array in one reaction in less than 12 hours. Compared to the glass-based, high-density microarray, the membrane-based macroarray offers a cost-efficient and flexible platform and, therefore has been adopted by many disease diagnosis development projects (Maoka et al., *Plant Dis.* 94, 1248-1254 (2010)). Moreover, macroarray results can be visualized with an unaided eye, which offers simplicity compared to microarrays. Recently, the application of chromogenic technology in macroarrays has further increased their versatility for use in laboratories or diagnostic labs with limited resources (Abdullahi et al., *J. Virol. Methods* 160, 90-100 (2009)).

Like other DNA diagnostic array technologies, macroarrays combine the advantage of two molecular biological advancements. First, the growing amount of DNA sequences available in publicly accessible databases (e.g., GenBank) allows for creation of signature probes specific to a species or infra-species target. Second, the high throughput capacity of the array technology permits hundreds of DNA oligomers to be queried simultaneously and produces signals indicative of matches between the oligomer and the query. The macroarray technique has been applied in a variety of areas. For example, in human biology it has been used for identification of different mRNA species present in human ejaculated spermatozoa (Dadoune et al., *Mol. Hum. Reprod.* 11, 133-140 (2004)) and in diagnosing ovarian cancer in epithelial cells (Chatterjee et al., *Cancer Res.* 66, 1181-1190 (2006)); while in veterinary science, macroarrays have been used for monitoring the Crimean-Congo Hemorrhagic fever virus, a tickborne zoonotic virus found across Africa, Eastern Europe and Asia (Wolfel et al., *J. Clin. Microbiol.* 47, 1025-1030 (2009)). In plant pathology, membrane-based DNA arrays have been used for detection, identification, monitoring and quantification of phytopathogenic agents (Fessehaie et al., *Phytopathology* 93, 262-269 (2003); Sholberg et al., *Plant Dis.* 89, 1143-1150 (2005)), such as phytopathogenic bacteria on potato, pathogens of apples, and pathogenic viruses and fungi in different host plants. At the infra-species level, DNA diagnostic arrays have been used for identification of races and biotypes of *Fusarium oxysporum* f. sp. *vasinfectum* on cotton and the detection of members of the *F. solani* species complex in solanaceous crops (Zhang et al., *Plant Dis.* 91, 1612-1620 (2007)).

Probe design is the first step in the development of a diagnostic array. Parameters such as probe length and annealing

temperatures (or GC content) play a role in array performance that have great impact on the fidelity of the assay, particularly with regard to the level of specificity and sensitivity attained (Barad et al., *Genome Res.* 14, 2486-2494 (2004); Goff et al., *RNA Biology* 2, E9-E16 (2005); Loy et al., *Clin. Chim. Acta* 363, 106-119 (2006)). If probes are not optimized for specificity, arrays may generate false positives due to cross-hybridization to similar sequences. On the other hand, high stringency often results in reduced signal intensity and may lead to false negatives. The occurrence of false positives and negatives is problematic because it is difficult to envisage whether a probe will attach efficiently to its target sequence and yield a good hybridization signal based on the sequence information alone (Li et al., *Bioinformatics* 17, 1067-1076 (2001); Chou et al., *Nucleic Acids Res.* 32, e99 (2004)). The design of effective probes is a challenge especially in related species where there is a high degree of sequence similarities. Scientists have therefore resulted to engineering redundancy into the DNA array's systems to improve accuracy and analytical power simply by over-representation. That is, using multiple probes per target to achieve reliable and accurate detection.

A number of studies have been able to achieve high levels of specificity with DNA arrays, but sensitivity has remained elusive (Wong et al., *Genome Biol.* 8, R93 (2007)), which made it difficult to detect species that were present at very low concentrations.

Increasing probe length can increase the array sensitivity, but specificity is often sacrificed. However, the impact of doubling (dimer) or tripling (trimer) a short probe sequence (about 20 nt monomer) to maintain the array specificity has not been addressed.

The objectives of this study were to develop a novel technical approach that could increase the sensitivity of a macroarray to enhance its early pathogen detection power, and which could maintain the macroarray detection specificity to ensure accurate pathogen identification. In this study, we designed and compared the performance of monomers, monomers with a ten-adenine tail (M-A10), monomers with 20 adenine tail (M-A20), dimers, and dimers with a ten-adenine spacer (DA), using a membrane-based macroarray platform (FIG. 1). It was hypothesized that (1) Dimeric oligonucleotide probes would be more sensitive than monomeric probes, (2) Poly-A spacer and tails would increase sensitivity of the probes, and that (3) Monomeric and dimeric probes would have equal specificity. Probes tested in this study were based on four important microbial pathogens of cereals, turfgrass and other plants—*Rhizoctonia solani* (basidiomycete), *Pythium aphanidermatum* (oomycete), *Fusarium solani* (ascomycete) and *F. oxysporum* (ascomycete) that cause brown patch, Pythium blight, root and vascular diseases, respectively.

Rapid and early diagnosis of microbe-causing diseases requires a technique capable of detecting low quantity of causal agents from the natural host environment. Accordingly, described herein is an improved macroarray detection technique that provides enhanced and consistent signals of detection with small reductions in specificity. The tandem-repeat dimeric probes (40-48 nt) had significantly higher sensitivity and lower signal variability compared to the monomers (20-24 nt).

The diagnostic array technique for microbe detection demands both high sensitivity and specificity. While developing macroarrays for the detection of solanaceous plant pathogens, Zhang et al. (2007) optimized the hybridization temperature to reduce cross-hybridization. However, this improvement in specificity came with a considerable sacrifice in signal intensity, which is also determined by the probe

length. Long sequence probes can decrease the array specificity. The hypothesis that dimeric probes containing two short identical sequences would enhance the DNA array sensitivity without sacrificing the specificity was tested. However, two monomers in tandem might interfere with hybridization of targets to the two matching sequences. Thus, the possibility that addition of a spacer in between may facilitate the binding of long target DNA fragments to the probes without unnecessary tangling was tested. However, the results showed that overall, dimers with poly-A spacer did not produce stronger signals than the dimers. This suggests that the proximity of two monomers to each other does not have a significant effect on hybridization. Previous work has shown that addition of spacers can have a large effect on hybridization signals for 15-30 mer oligonucleotide probes (Shchepinov et al., Nucleic Acids Res. 25, 1155-1161 (1997); Southern et al., Nature Genet., 21, 5-9 (1999); Guo et al., Nat. Biotechnol. 15, 331-335 (1997)).

To assess the reproducibility of the results, eleven sets of probes for DA, D, and M types (two to three independent sets for each of the four species) in addition to the controls were examined in this study. For the diagnostic arrays, multiple probes for each target species also ensures positive detection of genetically diverse target species. Random signal variation (noise) and the systematic deviation of the measurement from the true signal due to probe specific or other confounding technical effects can interfere with the results. Signal variation, expressed as a coefficient of variation (CV), showed that dimer probes had lowest variation while the monomers showed wide variability. Based on the statistical principles of sampling, the smaller the CV for the hybridization signals, the more reliable or reproducible the results are (Chou et al., 2004). This implies that fewer probes are needed when using dimer probes.

Although dimeric probes provided a low measurement variation and superior signal intensity, some dimeric probes tested here were relatively poor in discriminating sequences with high level of similarity (especially 1 nt differences). Cross-homology is a predictor of cross-hybridization. The concept of using dimers as probes does not change the level of similarity compared to the monomers. Therefore, the cross-hybridization observed maybe a consequence of other factors such as the binding energy accruing from longer probes. Longer probes typically have higher binding energy than shorter probes. Cross-hybridization observed here was only limited to members of the same genus and occurred in highly similar sequences where the mismatch base was located near the end or in a chain of the same base. This should be preventable in future array probe designs by avoiding such regions of a gene. These results showed that in all cases, the dimeric probes were able to distinguish strains that differed from the target by 3 or more nucleotides. Full discrimination also achieved for most cases of 2-nucleotide mismatches and one case of single nucleotide match. Therefore, with improved probe design strategy as described, the dimer array system is expected to distinguish between closely related pathogens, at species and infra species levels, such as race and subspecies.

Even though this macroarray system displayed some false-positives, it was remarkable in detecting low quantities of pathogen DNA. The dimer probes were able to detect as low as 0.1 pg target DNA in raw or mixed biological samples with plant extract despite the possibility of PCR bias in amplification. The dimers also reliably detected 0.01 fg target DNA from pure cultures on the array, while gel electrophoresis required a thousand fold more DNA for a positive detection. Assessment of low concentrations of target DNA that is only

present in few plant cells can be very elusive. Understanding pathogen biology is of paramount importance in disease diagnosis, since some pathogens are localized in certain parts of the tissue, while others are systemic in nature or cause symptoms in advance of tissue pathogen ingress. Visualization of pathogen structures using dissecting microscope to locate tissue with signs of the disease followed by targeted isolation of DNA from these tissues may improve the power of molecular detection.

In summary, reported herein is the finding that dimeric probes (e.g., 40-48 nt) enhance macroarray performance. The optimized dimer macroarray system demonstrated significantly higher sensitivity and consistency than the conventional monomer oligonucleotide arrays. Its detection sensitivity is also higher than many other currently available molecular diagnostic methods, such as PCR and real-time PCR. Moreover, this method is faster (less than 12 hours) than the traditional culture-based diagnostic method, which often takes days or even weeks. Therefore, this technique should be useful for early disease diagnosis when only trace amounts of target microbes are present in a sample. These findings should aid in the development of a multiplex diagnostic macroarray system to facilitate early disease diagnosis and management. The technique also can be adapted and applied to microbial ecological studies and other research areas.

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, made of monomers (nucleotides) containing a sugar, phosphate and a base that is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues.

The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single-stranded or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid," "nucleic acid molecule," or "polynucleotide" are used interchangeably.

Certain embodiments of the invention encompass isolated or substantially purified nucleic acid compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or RNA molecule is a DNA molecule or RNA molecule that exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or RNA molecule may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule is substantially free of other cellular material or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived.

The following terms are used to describe the sequence relationships between two or more nucleotide sequences: (a)

"reference sequence," (b) "comparison window," (c) "sequence identity," (d) "percentage of sequence identity," and (e) "substantial identity."

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well-known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller (Myers and Miller, CABIOS, 4, 11 (1988)); the local homology algorithm of Smith et al. (Smith et al., *Adv. Appl. Math.*, 2, 482 (1981)); the homology alignment algorithm of Needleman and Wunsch (Needleman and Wunsch, *JMB*, 48, 443 (1970)); the search-for-similarity-method of Pearson and Lipman (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA*, 85, 2444 (1988)); the algorithm of Karlin and Altschul (Karlin and Altschul, *Proc. Natl. Acad. Sci. USA*, 87, 2264 (1990)), modified as in Karlin and Altschul (Karlin and Altschul, *Proc. Natl. Acad. Sci. USA* 90, 5873 (1993)).

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, Calif.); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wis., USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al. (Higgins et al., CABIOS, 5, 151 (1989)); Corpet et al. (Corpet et al., *Nucl. Acids Res.*, 16, 10881 (1988)); Huang et al. (Huang et al., CABIOS, 8, 155 (1992)); and Pearson et al. (Pearson et al., *Meth. Mol. Biol.*, 24, 307 (1994)). The ALIGN program is based on the algorithm of Myers and Miller, supra. The BLAST programs of Altschul et al. (Altschul et al., *JMB*, 215, 403 (1990)) are based on the algorithm of Karlin and Altschul supra.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative

scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences. One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, less than about 0.01, or even less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g., BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix. Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein may be made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the program.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to a specified percentage of residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window, as measured by sequence comparison algorithms or by visual inspection. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather

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than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif.).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, or 94%, or even at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, 80%, 90%, or even at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5° C. lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1° C. to about 20° C., depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, or 94%, or even 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. In certain embodiments, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch (Needleman and Wunsch, JMB, 48, 443 (1970)). An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a

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second peptide, for example, where the two peptides differ only by a conservative substitution. Thus, certain embodiments of the invention provide nucleic acid molecules that are substantially identical to the nucleic acid molecules described herein.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. The thermal melting point (T_m) is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (1984); $T_m = 81.5^\circ C + 16.6 (\log M) + 0.41 (\% GC) - 0.61 (\% form) - 500/L$; where M is the molarity of monovalent cations, % GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1° C. for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with >90% identity are sought, the T_m can be decreased 10° C. Generally, stringent conditions are selected to be about 5° C. lower than the T_m for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4° C. lower than the T_m ; moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10° C. lower than the T_m ; low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20° C. lower than the T_m . Using the equation, hybridization and wash compositions, and desired temperature, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a temperature of less than 45° C. (aqueous solution) or 32° C. (formamide solution), the SSC concentration is increased so that a higher temperature can be used. Generally, highly stringent hybridization and wash con-

ditions are selected to be about 5° C. lower than the T_m for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72° C. for about 15 minutes. An example of stringent wash conditions is a 0.2×SSC wash at 65° C. for 15 minutes. Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1×SSC at 45° C. for 15 minutes. For short nucleotide sequences (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, less than about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30° C. and at least about 60° C. for long probes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2× (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids that have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.1×SSC at 60 to 65° C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37° C., and a wash in 1× to 2×SSC (20×SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55° C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37° C., and a wash in 0.5× to 1×SSC at 55 to 60° C.

In addition to the chemical optimization of stringency conditions, analytical models and algorithms can be applied to hybridization data-sets (e.g. microarray data) to improve stringency.

Certain embodiments of the invention will now be illustrated by the following non-limiting Examples.

EXAMPLE 1

Dimeric Oligonucleotide Probes Enhance Diagnostic Macroarray Performance

Disease management would be improved with more rapid and more accurate pathogen detection and identification techniques. Described herein is a macroarray diagnostic technique with enhanced detection sensitivity with only small reduction in specificity. With probes designed based on the internal transcribed spacer sequences of the rRNA genes of fungal and oomycete strains, a macroarray was produced that included five types of oligonucleotide probes: monomers (20-24 nt), dimers (40-48 nt), dimers with a poly-A spacer of 10 bases between the two repeats (50-58 nt), monomers with a poly-A tail of 10 (30-34 nt) and 20 (40-44 nt) bases. The use of repeat sequence probes (dimers) greatly improved the sensitivity of the macroarray. The dimeric probes could reliably detect 0.01 fg target genomic DNA, which is lower than the detection limits of most currently available molecular diagnostic methods, such as the conventional PCR and real-time

PCR. Dimer probes also had lower signal variability, thereby increasing the macroarray signal uniformity. However, in a few cases, specificity was reduced in the dimer probes. Cross-hybridization occurred in highly similar sequences where the mismatched base was located near the end or in a chain of the same base, but this should be prevented in future array probe design.

Probe Sensitivity

Dimers and DA had significantly higher sensitivity than those of the M, M-A10 and M-A20 (FIG. 3). To test whether the monomers were being outcompeted in the race for hybridization targets, monomers were printed on a separate membrane. Results showed that there was no significant difference in signal intensities between monomers printed on a separate array and monomers printed in same array with dimers (Table 5).

Signal Uniformity

Signal intensities of monomeric probes were most variable compared to the other types of probes (FIG. 2, FIG. 4). The signal intensities for monomers were so diverse that *F. oxysporum* had one probe with an inverted gray value of 89 while the other was showing only 4. On the same array, dimers and dimers with poly-A spacer derived from those monomers had lesser inverted gray value disparity (117-108 and 117-114, respectively). The coefficient of variation (CV), defined here as the standard deviation divided by the means of the hybridization signals was used as a measure of the variation of signal intensity (Chou et al., 2004; FIG. 4). Overall, the dimers displayed the lowest variability, followed by the dimers with poly-A and then the monomers M-A20 and M-A10. Monomers alone had the greatest variability.

Limit of Detection and Validation

The dimer probes could reliably detect up to 0.01 fg genomic DNA, which is a thousand times lower than using PCR product visualization with gel electrophoresis (FIG. 5). A simulation based on a condition where the pathogen DNA was serially diluted while holding the host grass DNA at 1 ng showed that dimeric probes could detect target DNA at all levels tested (Table 3), including 0.1 pg at a ratio of 1:10⁴ pathogen to host DNA for *R. solani* and *P. aphanidermatum*. Mixing the DNA of the target species, commonly found co-inhabiting fungal species and the host plant did not interfere with the hybridization reactions for all reactions tested (Table 3). The macroarray was also successfully validated with target species infected plant or soil materials. The array detection and identification results matched with the identification based on traditional microscopic observation, culture isolation and ITS DNA sequence (Table 1).

Array Specificity

There was no cross hybridization to *P. aphanidermatum* and *R. solani* probes from any of the non-target isolates. Cross-hybridization was observed in three sets of dimers and DA probes (Table 6) when reacting with non-target species that had one or two nucleotide sequence mismatches (Table 4). The mismatches between the cross-hybridized probes and the corresponding non-target sequences were located either in chain of A or G (*F. solani* #F19/probe Fs6 and *F. equiseti* #S2/probe Fo1, Tables 4) or near the end of the probe sequence (*F. solani* #F3/probe Fs13). The cross-hybridization signal intensity values were 44% or lower compared to the perfect-match signals. False negatives were only observed in a monomer probe for *P. aphanidermatum* (Table 6).

Materials and Methods

Isolates

Test isolates used in this study are listed in Table 1. The identity of the target species, *P. aphanidermatum* and *R. solani*, was confirmed by morphology and the internal tran-

scribed spacer sequences of the rRNA genes (ITS), while the *Fusarium* species were characterized in another study by partial sequences of translation elongation factor-1 α (EF-1 α), ITS, and β -tubulin (TUB) genes. In addition, non-target species of *Pythium*, *Rhizoctonia*, and *Fusarium* were used to test the array specificity. Three common co-inhabiting fungi in turfgrass soil, *Curvularia trifolii*, *Trichoderma virens*, and *Mortierella elongata* were also included in the study for validation and cross-reaction tests.

200 μ M each of the dNTPs, 0.5 μ M of each forward and reverse primers, and 0.5 U Taq polymerase. The thermal cycling parameters were 95° C. for 5 min; 35 cycles of 95° C. for 1 min, 56° C. for 1 min., and 72° C. for 1 min; followed by 5 10 min at 72° C. PCR products were purified according to the manufacturer's protocol using the QIAquick PCR Purification Kit (Qiagen), quantified using NanoVue spectrophotometer and sequenced when identity of the isolates needed to be confirmed. Sequencing of the purified ITS PCR products was

TABLE 1

Microbial, host species and substrate used for testing and validating the macroarray in this study				
Microbial/host species	Collection ID	Host/substrate	Origin	GenBank accession
<u>Fungi-Zygomycota</u>				
<i>Mortierella elongata</i>	#141	<i>Poa annua</i>	Denville, NJ	—
<u>Fungi-Ascomycota</u>				
<i>Curvularia trifolii</i>	#185	<i>Agrostis</i> sp.	New Brunswick, NJ	—
<i>Fusarium equiseti</i>	#S2	turfgrass soil	New Brunswick, NJ	—
<i>F. oxysporum</i>	#F2 (NRRL 54168)	<i>Lilium longiflorum</i> bulbs	New Brunswick, NJ	HQ379648
<i>F. oxysporum</i>	#S4	turfgrass soil	New Brunswick, NJ	—
<i>F. solani</i>	#F3 (NRRL 54169)	<i>Lilium longiflorum</i> bulbs	New Brunswick, NJ	HQ379661
<i>F. solani</i>	#F19 (NRRL 54185)	<i>Lilium longiflorum</i> bulbs	New Brunswick, NJ	HQ379663
<i>Trichoderma virens</i>	#126-L	<i>Agrostis stolonifera</i>	New Brunswick, NJ	—
<u>Fungi-Basidiomycota</u>				
<i>Rhizoctonia solani</i>	#RH 20	unknown	State College, PA	—
<i>R. solani</i>	#98	<i>Lolium multiflorum</i>	New Brunswick, NJ	—
<i>Waitea circinata</i> var. <i>circinata</i>	#10	<i>Agrostis</i> sp.	NJ	—
<i>W. circinata</i> var. <i>circinata</i>	#158	<i>Agrostis</i> sp./ <i>Poa</i> sp.	Bedminster, NJ	HQ166071
<i>W. circinata</i> var. <i>zeae</i>	#1	<i>Poa annua</i>	New Brunswick, NJ	—
<u>Stramenopiles-Oomycota</u>				
<i>Pythium aphanidermatum</i>	#60	<i>Festuca arundinacea</i>	NJ	—
<i>P. aphanidermatum</i>	#99	<i>Lolium multiflorum</i>	New Brunswick, NJ	—
<i>P. rostrum</i>	#123p	<i>Agrostis</i> sp.	New Brunswick, NJ	—
<i>P. torulosum</i>	#122	<i>Poa annua</i>	New Brunswick, NJ	—
<i>P. volutum</i>	#124p-1	<i>poa annua</i>	New Brunswick, NJ	—
<u>Host/substrate</u>				
^a	#199	<i>Agrostis stolonifera</i>	New Brunswick, NJ	—
^b	NA	<i>Poa annua</i>	New Brunswick, NJ	—
^c	#176	<i>Poa annua</i>	New Brunswick, NJ	—
^d	NA	Soil	New Brunswick, NJ	—

NRRL = Agricultural Research Service Culture Collection (NCAUR, Peoria, IL).

^a*Agrostis stolonifera* with symptoms of brown patch.

^bAsymptomatic, disease free *Poa annua* from greenhouse.

^c*Poa annua* with symptoms of *Pythium* blight.

Soil substrates used were those associated with *P. aphanidermatum* and *R. solani*.

NA = Not available.

DNA Extraction, Amplification, Purification and Sequencing

Genomic DNA from all microbial isolates was extracted from 1- to 2-week-old cultures growing on PDA plates (Difco laboratories, Detroit, Mich.) using the UltraClean Soil DNA kit (MoBio Laboratories Inc., Solana Beach, Calif., USA) or DNeasy Plant Mini kit (Qiagen Inc., Valencia, Calif., USA), following the manufacturer's protocol. The extracted genomic DNA was quantified using a NanoVue spectrophotometer (GE Healthcare Bio-Sciences Corp., Piscataway, N.J., USA) and diluted to 5 ng/ μ l before PCR. The ITS region was amplified with primers ITS1 and ITS4 (White et al., In: Innis et al. (Eds.), PCR Protocols: A Guide to Methods and Applications. Academic Press, New York, pp. 315-322 (1990)). PCR was carried out in a 25 μ l reaction volume containing 3 μ l (15 ng) genomic DNA, 1xPCR buffer (Applied Biosystems, Foster City, Calif., USA), 1.5 mM MgCl₂,

50 run on an Applied Biosystems 3730xl sequencer by GENEWIZ (GENEWIZ, Inc., South Plainfield, N.J., USA). Oligonucleotide Probe Design and Array Development

Two sets of probes, dimers and dimers with a poly-A10 spacer of 10 bases for the four target species and the controls 55 (Table 2) were designed based in part on 20-24 nt oligomer probes previously designed and validated by Lievens et al. (2003), Saiki et al., Proc. Natl. Acad. Sci. USA 86, 6230-6234. (1989), and Zhang et al., (2007, 2008). Accordingly, certain embodiments of the invention are directed to these 60 probes. M-A10 and M-A20 were designed for *P. aphanidermatum* and *F. solani* only (Table 2), since we were more interested with the effect of duplexing but at the same time we wanted to disqualify sequence length as the only factor contributing to the enhanced sensitivity. The performance of the macroarray that contained the five types of probes was tested against the macroarray that contained only the monomeric probes.

The macroarray development followed the procedure described by Zhang et al. (2007). Briefly, 20 µmol of each detector oligonucleotide probe was spotted onto Hybond N+ nylon membranes (GE Healthcare Bio-Sciences Corp., Piscataway, N.J., USA) in quadruplicate using a 96-pin tool (V&P Scientific Inc., San Diego, Calif., USA). Three types of controls were also spotted. First, the positive controls included the ITS4 primer, which is a universal primer for both fungi and oomycetes, and ITS2, which is a fungal universal primer (Table 2). Second, internal controls that differed from

ITS2 at two bases were also spotted on the membrane. Negative controls were sterile water and the spotting buffer. The positive and internal controls also constituted dimers, DA, M-A10 and M-A20. The spotted membranes were air dried for 10 min and then fixed by UV exposure at 240 mJ/cm². After incubation in a 0.5% sodium dodecyl sulfate (SDS) solution at 60° C. for an hour, membranes were rinsed in 100 mM Tris (pH 8.0) for 5 min, and kept moist at 4° C. until used. This last step was also used for stripping the array.

TABLE 2

Probe name, type, sequence, length and targeted species used in this study.						
Probe name	Probe type ^a	Probe sequence	Reference ^b	Length	Probe	Length Probe target
<u>Specific target probe</u>						
Pa1	M	GGAGAGAGATGGCAGAATGTGAG (SEQ ID NO: 1)	Saiki et al. 1989	23	P. aphanidermatum	
Pa2	M	GGGAGAGAGATGGCAGAATGTGAG (SEQ ID NO: 2)	Saiki et al. 1989	24	P. aphanidermatum	
Pa3	M	GAGGTGTACCTGAATTGTGTGAGG (SEQ ID NO: 3)	Saiki et al. 1989	24	P. aphanidermatum	
Pa1R	D	GGAGAGAGATGGCAGAATGTGAGGGAGAGAGATGGCAGAATGTGAG (SEQ ID NO: 4)		46	P. aphanidermatum	
Pa2R	D	GGGAGAGAGATGGCAGAATGTGAGGGAGAGAGATGGCAGAATGTGAG AG (SEQ ID NO: 5)		48	P. aphanidermatum	
Pa3R	D	GAGGTGTACCTGAATTGTGTGAGGGAGGTGTACCTGAATTGTGTGAG GG (SEQ ID NO: 6)		48	P. aphanidermatum	
Pa1R-A	DA	GGAGAGAGATGGCAGAATGTGAGAAAAAAAAAAAGGAGAGAGATGGCAGAATGTGAG (SEQ ID NO: 7)		56	P. aphanidermatum	
Pa2R-A	DA	GGGAGAGAGATGGCAGAATGTGAGAAAAAAAAAAAGGGAGAGAGATGGCAGAATGTGAG (SEQ ID NO: 8)		58	P. aphanidermatum	
Pa3R-A	DA	GAGGTGTACCTGAATTGTGTGAGGAAAAAAAAGAGGTGTACCTGAATTGTGTGAGG (SEQ ID NO: 9)		58	P. aphanidermatum	
Pa1-A10	M-A10	GGAGAGAGATGGCAGAATGTGAGAAAAAAAAAA (SEQ ID NO: 10)		33	P. aphanidermatum	
Pa2-A10	M-A10	GGGAGAGAGATGGCAGAATGTGAGAAAAAAAAAA (SEQ ID NO: 11)		34	P. aphanidermatum	
Pa3-A10	M-A10	GAGGTGTACCTGAATTGTGTGAGGAAAAAAA (SEQ ID NO: 12)		34	P. aphanidermatum	
Pa1-A20	M-A20	GGAGAGAGATGGCAGAATGTGAGAAAAAAAAAAAAAAA (SEQ ID NO: 13)		43	P. aphanidermatum	
Pa1-A20	M-A20	GGGAGAGAGATGGCAGAATGTGAGAAAAAAAAAAAAAAA (SEQ ID NO: 14)		44	P. aphanidermatum	
Pa3-A20	M-A20	GAGGTGTACCTGAATTGTGTGAGGAAAAAAA (SEQ ID NO: 15)		44	P. aphanidermatum	
Rs2	M	CAGTGTATGCTGGTTCCACTC (SEQ ID NO: 16)	Zhang et al. 2008	23	R. solani	
Rs3	M	TGTTGAAACTTAGTATTAGATGCGT (SEQ ID NO: 17)	Zhang et al. 2008	23	R. solani	
Rs4	M	GAGTGGAACCAAGCATAACACTG (SEQ ID NO: 18)	Zhang et al. 2008	23	R. solani	

TABLE 2-continued

Probe name, type, sequence, length and targeted species used in this study.						
Probe name	Probe type ^a	Probe sequence	Reference ^b	Probe Length	Probe target	
Rs2R	D	CAGTGGTATGCTGGTCCACTCCAGTGTATGCTGGTCCACTC (SEQ ID NO: 19)		46	<i>R. solani</i>	
Rs3R	D	TGTTGAAACTTAGTATTAGATGCGTTGTTGAAACTTAGTATTAGAT GCGT (SEQ ID NO: 20)		46	<i>R. solani</i>	
Rs4R	D	GAGTGGAACCAAGCATAACACTGGAGTGGAACCAAGCATAACACTG (SEQ ID NO: 21)		46	<i>R. solani</i>	
Rs2R-A	DA	CAGTGGTATGCTGGTCCACTCAAAAAAAAACAGTGTATGCTT GGTTCACTC (SEQ ID NO: 22)		56	<i>R. solani</i>	
Rs3R-A	DA	TGTTGAAACTTAGTATTAGATGCGTAAAAAAAAATGTTGAAACTT AGTATTAGATGCGT (SEQ ID NO: 23)		56	<i>R. solani</i>	
Rs4R-A	DA	GAGTGGAACCAAGCATAACACTGAAAAAAAAAGAGTGGAACCAAG CATAACACTG (SEQ ID NO: 24)		56	<i>R. solani</i>	
Fs4	M	TCGCGTAGTAGCTAACACCTCGC (SEQ ID NO: 25)	Zhang et al. 2007	23	<i>F. solani</i>	
Fs6	M	CCTGTGAACATACCTAACCGTTG (SEQ ID NO: 26)	Zhang et al. 2007	23	<i>F. solani</i>	
Fs13	M	TTATACAACACTCATCAACCCTGTGA (SEQ ID NO: 27)	Zhang et al. 2007	24	<i>F. solani</i>	
Fs4R	D	TCGCGTAGTAGCTAACACCTCGCTCGCGTAGTAGCTAACACCTCGC (SEQ ID NO: 28)		46	<i>F. solani</i>	
Fs6R	D	CCTGTGAACATACCTAACCGTTGCTGTGAACATACCTAACCGTTG (SEQ ID NO: 29)		46	<i>E. solani</i>	
Fs13R	D	TTATACAACACTCATCAACCCTGTGATTATACAACCTCATCAACCCTGT GA (SEQ ID NO: 30)		48	<i>F. solani</i>	
Fs4R-A	DA	TCGCGTAGTAGCTAACACCTCGCAAAAAAAATCGCGTAGTAGCT AACACTCGC (SEQ ID NO: 31)		56	<i>F. solani</i>	
Fs6R-A	DA	CCTGTGAACATACCTAACCGTTGAAAAAAACCTGTGAACATAC CTAACCGTTG (SEQ ID NO: 32)		56	<i>F. solani</i>	
Fs13R-A	DA	TTATACAACACTCATCAACCCTGTGAAAAAAATTATACAACCTCA CTAACCCCTGTGA (SEQ ID NO: 33)		58	<i>F. solani</i>	
Fs4-A10	M-A10	TCGCGTAGTAGCTAACACCTCGCAAAAAAAA (SEQ ID NO: 34)		33	<i>F. solani</i>	
Fs6-A10	M-A10	CCTGTGAACATACCTAACCGTTGAAAAAAA (SEQ ID NO: 35)		33	<i>F. solani</i>	
Fs13-A10	M-A10	TTATACAACACTCATCAACCCTGTGAAAAAAA (SEQ ID NO: 36)		34	<i>F. solani</i>	
Fs4-A20	M-A20	TCGCGTAGTAGCTAACACCTCGCAAAAAAAA (SEQ ID NO: 37)		43	<i>F. solani</i>	
Fs6-A20	M-A20	CCTGTGAACATACCTAACCGTTGAAAAAAA (SEQ ID NO: 38)		43	<i>F. solani</i>	
Fs13-A20	M-A20	TTATACAACACTCATCAACCCTGTGAAAAAAA (SEQ ID NO: 39)		44	<i>F. solani</i>	
Fo1	M	CGTTCTCAAATTGATTGGCGGT (SEQ ID NO: 40)	Zhang et al. 2008	24	<i>F. oxysporum</i>	

TABLE 2-continued

Probe name, type, sequence, length and targeted species used in this study.						
Probe name	Probe type ^a	Probe sequence	Reference ^b	Probe Length	Probe target	
Fox2	M	GTTGGGACTCGCGTTAACCG (SEQ ID NO: 41)	Lievens et al. 2003	21	<i>F. oxysporum</i>	
Fo1R	D	CGTTCCTCAAATTGATTGGCGGTCCGTTCTCAAATTGATTGGCGG TC (SEQ ID NO: 42)		48	<i>F. oxysporum</i>	
Fox2R	D	GTTGGGACTCGCGTTAACCGGGACTCGCGTTAACCG (SEQ ID NO: 43)		42	<i>F. oxysporum</i>	
Fox2-A	DA	CGTTCCCAAATTGATTGGCGGTCAAAAAAAAAACGTTCTCAAAT TGATTGGCGGT (SEQ ID NO: 44)		58	<i>F. oxysporum</i>	
Fo1R-A	DA	GTTGGGACTCGCGTTAACCGAAAAAAAGTTGGGACTCGCGTT AATTGCG (SEQ ID NO: 45)		52	<i>F. oxysporum</i>	
<u>Positive control Probe</u>						
ITS2	M	GCTGCGTTCTTCATCGATGC (SEQ ID NO: 46)	White et al. 1990	20	Fungi	
ITS4	M	TCCTCCGCTTATTGATATGC (SEQ ID NO: 47)	White et al. 1990	20	Fungi & oomycete	
ITS2R	D	GCTGCGTTCTTCATCGATGCCTGCGCTGCGTTCTTCATCGATGC (SEQ ID NO: 48)		40	Fungi	
ITS4R	D	TCCTCCGCTTATTGATATGCCTCCGCTTATTGATATGC (SEQ ID NO: 49)		40	Fungi & oomycete	
ITS2R-A	DA	GCTGCGTTCTTCATCGATGCAAAAAAAAAGCTGCGTTCTTCATCG ATGC (SEQ ID NO: 50)		50	Fungi	
ITS4R-A	DA	TCCTCCGCTTATTGATATGCAAAAAAAAATCCTCCGCTTATTGAT ATGC (SEQ ID NO: 51)		50	Fungi & oomycete	
ITS2-A10	M-A10	GCTGCGTTCTTCATCGATGCAAAAAAAAA (SEQ ID NO: 52)		30	Fungi	
ITS4-A10	M-A10	TCCTCCGCTTATTGATATGCAAAAAAAAA (SEQ ID NO: 53)		30	Fungi & oomycete	
ITS2-A20	M-A20	GCTGCGTTCTTCATCGATGCAAAAAAAAAAAAAAA (SEQ ID NO: 54)		40	Fungi	
ITS4-A20	M-A20	TCCTCCGCTTATTGATATGCAAAAAAAAAAAAAAA (SEQ ID NO: 55)		40	Fungi & oomycete	
<u>Internal control Probe</u>						
ITS2-2-1	M	GCTGCGTTGATCATCGATGC (SEQ ID NO: 56)	Zhang et al. 2008	20	None	
ITS2-2-1R	D	GCTGCGTTGATCATCGATGCCTGCGTTGATCATCGATGC (SEQ ID NO: 57)		40	None	
ITS2-2-1R-A	DA	GCTGCGTTGATCATCGATGCAAAAAAAAAGCTGCGTTGATCATCG ATGC (SEQ ID NO: 58)		50	None	

TABLE 2-continued

Probe name, type, sequence, length and targeted species used in this study.					
Probe name	Probe type ^a	Probe sequence	Reference ^b	Probe Length	Probe target
ITS2-2-1-A10	M-A10	GCTGCGTTGATCATCGATGCAAAAAAAAAAAA (SEQ ID NO: 59)		30	None
ITS2-2-1-A20	M-A20	GCTGCGTTGATCATCGATGCAAAAAAAAAAAAAAA (SEQ ID NO: 60)		40	None

^aD = dimer, DA = dimer with 10 adenine nucleotides(poly-A) spacer, M = monomer, M-A10 = monomer with 10 adenine nucleotides (poly-A10) tail and M-A20 = monomer with 20 adenine nucleotides(poly-A20) tail.

^bReference for literature citations. Oligonucleotide probes that do not have a reference were modifications from referenced probes by the authors for this study.

Hybridization

Hybridization was carried out as described previously (Zhang et al., 2007, 2008). The test ITS amplicons from either target or non-target materials were labeled and hybridized using the Gene Images AlkPhos Direct Labeling (GE Healthcare Bio-Sciences Corp., Piscataway, N.J., USA) and Detection System with CDP-Star (Topix Inc., Bedford, Mass., USA). Before use, the arrays were pre-hybridized at 55° C. for 15 min and hybridized with 100 ng (10 µl of 10 m/µl) of labeled ITS amplicon at 55° C. for 2 h. After two primary washes and two secondary washes, the detection reagent was added to the array to react for an hour, followed by 30 min of film exposure. Chemiluminescence was detected using Kodak Biomax Light film. Developed films were scanned by an Aficio MP C6000 Color Copier/Scanner (Ricoh Americas Corporation, West Caldwell, N.J., USA) and read with ImageJ 1.33u (National Institutes of Health, MD, USA).

Array Sensitivity

The signal intensity for hybridization was measured as the average inverted gray value for the quadruplicate spots for each detector oligonucleotide on the array after the back-

20 hybridization was conducted as described above. Ten µl of purified ITS PCR product was used for hybridization and gel electrophoresis. The experiments were conducted twice. To determine whether DNA from the host and other co-inhabiting fungi would interfere with the target species detection, the target DNA was 10x serially diluted (from 1 ng/µl to 1×10⁻⁴ ng/µl) and mixed with 1 ng of plant DNA. Two µl of the mixture were used for PCR amplification in a 25 µl reaction mix (Table 3). Plant DNA was derived from clean greenhouse grown *Poa annua* with no history of disease infection. Serially diluted genomic DNA of the target species (from 1 ng/µl to 1×10⁻² ng/µl of #98 or #99) was mixed in same ratio with the serially diluted genomic DNA from three common turf-grass-associated fungi, *C. trifolii*, *T. virens*, and *M. elongata* 25 (Table 3). PCR amplification and hybridization were done as explained above. Control experiments were done to test if the observed results were due to skewed amplification by PCR, by mixing 2.5 ng of purified PCR products of each of the test sample (*P. annua*, *C. trifolii*, *T. virens*, *M. elongata*, and the target species) to final volume of 10 µl before macroarray hybridization.

TABLE 3

Amount of target species DNA, common co-inhabiting non-target fungal species DNA, and host DNA used in 25 µl-PCR reactions for assessment of hybridization interference						
Reaction number	Target DNA amount (ng) ^a	<i>C. trifolii</i> DNA amount (ng)	<i>M. elongata</i> DNA amount (ng)	<i>T. virens</i> DNA amount (ng)	Host DNA amount (ng)	Hybridization signal observed ^b
1	10 ⁻⁴	0	0	0	1	yes
2	10 ⁻³	0	0	0	1	yes
3	10 ⁻²	0	0	0	1	yes
4	10 ⁻¹	0	0	0	1	yes
5	10 ⁻²	10 ⁻²	10 ⁻²	10 ⁻²	1	yes
6	10 ⁻¹	10 ⁻¹	10 ⁻¹	10 ⁻¹	1	yes
7	1	1	1	1	1	yes

^a Target species used were *Rhizoctonia solani* isolate #98 or *Pythium aphanidermatum* isolate #99. The non-target fungal species used were *Curvularia trifolii*, *Trichoderma virens*, and *Mortierella elongata* while the host species was *Poa annua*.

^b Yes implies that a hybridization signal was observed.

ground gray values were subtracted. Since in 8-bit grayscale images, the darkest picture corresponds to the lowest value, each value was inverted by subtracting its reading from 255 (i.e. inverted gray value=255-gray value readings). Each experiment was conducted at least twice. The signal intensity of the monomers was compared vis-à-vis those of the dimer, DA and where applicable, M-A10 and M-A20 for each isolate.

Two isolates, *R. solani* (#98) and *P. aphanidermatum* (#99), were used to determine the detection limit of the PCR-coupled macroarray method. The genomic DNA of #98 and #99 was 10x serially diluted from 1 ng/µl to 1×10⁻¹⁰ ng/µl prior to a standard ITS PCR. Following ITS amplification,

55 Array Validation

The macroarray was validated with DNA extracted from plant tissues or soils infested by the target species. DNA was extracted using UltraClean Soil DNA kit (MoBio Laboratories, Inc., Solana Beach, Calif., USA) or DNeasy Plant Mini kit (Qiagen Inc., Valencia, Calif., USA) depending on the material. Microscopic observation was also performed to check for presence of fungal or oomycete structures in the substrate.

60 Array Specificity

To assess the specificity of detection by the array, fungal and oomycete strains that differ from the target species by 1 to 3 bases of the probe sequence were tested for cross-reaction against the array (Table 4). DNA extraction, purification and

hybridization were done as described above. Other fungal and oomycete species often found associated with turfgrasses

were also included in the experiments to test the array's ability to discriminate non-target species.

TABLE 4

DNA sequence mismatches between target and closely related non-target species at the ITS region where the probe was designed.				
Target Species ^b	Probe	Probe sequence	Non-target ^a Species with 1 nt mismatch	Mismatch position
Pa	Pa1	GGAGAGAGATGGCAGAATGTGAG (SEQ ID NO: 1)	<i>P. torulosum</i> (#122)	GGAGAGAA <u>A</u> TGGCAGAATGTGAG (SEQ ID NO: 61)
	Pa2	GGGAGAGAGATGGCAGAATGTGAG (SEQ ID NO: 2)	—	NA
	Pa3	GAGGTGTACCTGAATTGTGTGAGG (SEQ ID NO: 3)	—	NA
Rs	Rs2	CAGTGTATGCTTGGTTCCACTC (SEQ ID NO: 16)	—	NA
	Rs3	TGTTGAAACTTAGTATTAGATGCGT— (SEQ ID NO: 17)	—	NA
	Rs4	GAGTGGAACCAAGCATAACACTG (SEQ ID NO: 18)	—	NA
Fs	Fs4	TCGCGTAGTAGCTAACACCTCGC (SEQ ID NO: 25)	—	NA
	Fs6	CCTGTGAACATACCTAAACGTTG (SEQ ID NO: 26)	<i>F. solani</i> (#F19)	CCTGTGAACATAC <u>CTAA</u> ACGTTG (SEQ ID NO: 67)
	Fs13	TTATACAACTCATCAACCCTGTGA (SEQ ID NO: 27)	<i>F. solani</i> (#F3)	TTATT <u>CA</u> ACTCATCAACC <u>CTGTGA</u> (SEQ ID NO: 69)
Fo	Fo1	CGTTCCCTCAAATTGATTGGCGGTG (SEQ ID NO: 40)	—	NA
	Fo2	GTTGGGACTCGCGTTAATTG (SEQ ID NO: 41)	—	NA
Target Species ^b	with 2 nt mismatch	Species with 3 nt mismatch	Species with 3 nt mismatch	Mismatch positions
Pa	<i>P. volutum</i> (#124p-1)	GGAGAGAA <u>A</u> ATGGCAGAATGTGAG (SEQ ID NO: 62)	—	NA
	<i>P. torulosum</i> (#122)	<u>A</u> GGAGAGAA <u>A</u> ATGGCAGAATGTGAG (SEQ ID NO: 63)	<i>P. volutum</i> (#124p-1)	<u>A</u> GGAGAGAA <u>A</u> ATGGCAGAATGTGAG (SEQ ID NO: 64)
	<i>P. volutum</i> (#124p-1), <i>P. torulosum</i> (#122)	GAGGTGTACCTGTCTGTGTGAGG (SEQ ID NO: 65)	—	NA
Rs	—	NA	—	NA
	—	NA	—	NA
	—	NA	—	NA
Fs	<i>F. equiseti</i> (#S2)	<u>T</u> AGCGTGAGTAGCTAACACCTCGT— (SEQ ID NO: 66)	—	NA
	<i>F. equiseti</i> (#S2)	CCTGTGAACATACCTACGTTG (SEQ ID NO: 68)	—	NA
	<i>F. oxysporum</i> (#F2, #S4), <i>F. equiseti</i> (#S2)	TTATACAACTCATCAA <u>ACCC</u> CTGT — GA (SEQ ID NO: 70)	—	NA

TABLE 4-continued

DNA sequence mismatches between target and closely related non-target species at the ITS region where the probe was designed.

Fo	<i>F. equiseti</i> (#S2)	CGTCCCTCAAAT <u>CGATTGGGGTC</u> - (SEQ ID NO: 71)	NA
-	NA	<i>F. equiseti</i> (#S2)	GTTGGGACTCGCGGTAA <u>CCCG</u> (SEQ ID NO: 72)

^aindicates no candidate species was available with the specified mismatch, NA = not applicable, sequences that caused cross-hybridization are in boldface.

^bPa = *Phythium aphanidermatum*, Rs = *Rhizoctonia solani*, Fs = *Fusarium solani*, Fo = *Fusarium oxysporum*

TABLE 5

Two-way ANOVA for hybridization results of monomers printed on a membrane with and without other probe types, tested against four isolates ($N = 24$).

ANOVA					
Source of Variation	SS	df	MS	F	P-value
Monomer type	192.13	1	192.13	0.21	0.65
Isolate	5154.76	3	1718.25	1.92	0.17

TABLE 5-continued

Two-way ANOVA for hybridization results of monomers printed on a membrane with and without other probe types, tested against four isolates ($N = 24$).

ANOVA						
	Source of Variation	SS	df	MS	F	P-value
20	Interaction (Monomer type x Isolate)	257.45	3	85.82	0.09	0.96
	Error	14349.09	16	896.82		
25	Total	19953.44	23			

TABLE 6

Comparison of hybridization results between target and non-target species based on monomer, dimer, and dimer with poly-A spacer probes.

Probe target species/type/name^c

TABLE 6-continued

Comparison of hybridization results between target and non-target species based on monomer, dimer, and dimer with poly-A spacer probes.

Pa	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Pr	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Pt	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Pv	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Wc	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Wc	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Rs	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Rs	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Tv	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

^aCt = *Curvularia trifoliae*, Fe = *Fusarium equiseti*, Fo = *Fusarium oxysporum*, Fs = *Fusarium solani*, Me = *Mortierella elongata*, Poa = *Poa annua*, Pa = *Pythium aphanidermatum*, Pr = *Pythium rostrum*, Pt = *Pythium torulosum*, Pv = *Pythium volutum*, Wc = *Waitea circinata* var. *circinata*, Rs = *Rhizoctonia solani*, Tv = *Trichoderma virens*.

^bCollection ID/accession number.

^cA list of 33 probe names derived from 4 target species and 3 probe types, where M = monomer, D = dimer, and DA = dimer with 10 adenine (poly-A) spacer.

^d- indicates no hybridization signal was observed, + indicates a hybridization signal was observed. All isolates were tested on three probes for each target in quadruplicate. False negatives (⊖) were observed in M probe PaI for *P. aphanidermatum* test isolates (#60 and #99). False positives (⊕) between *F. oxysporum* probes (D and DA) and *F. equiseti*, and between *F. solani* probes (D and DA) and non-target *F. solani* strains.

Statistical Analysis

Every probe was spotted four times on the macroarray and measured individually, and the hybridization experiment was repeated at least once. Quantitative data were analyzed using a two-way ANOVA (isolate and probe type) with SAS (version 9.2) statistical software. A P value <0.05 was considered significant. Specifically, signal intensities of hybridization of monomers printed on a membrane with and without other probe types were analyzed using a 2×4 factorial design.

20

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EXAMPLE 2

Additional Dimeric Oligonucleotide Probes

Additional dimeric probes that hybridize to target sequences that are specific to over 50 turf grass pathogens were designed as described in Example 1. The sequences for these probes, as well as the pathogenic target, are shown in Table 7. Positive and negative control probes are also included in this table. These probes may be evaluated and employed in macroarray analyses, as described above in Example 1.

TABLE 7

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
<i>Brumeria graminis</i>	Bg_2D	TGTAACCTCCCGTAGTAATATGTAACACTCTCCCGTAGTAATA (SEQ ID NO: 73)	44
	Bg_3D	GTTGACCCCTCACCCGTGTCGATTAGTTGACCCCTCACCCGTGTCGATTA (SEQ ID NO: 74)	50
	Bg_4D	AGGGTCCGTAACACCTCTCAAGCCTAGCGTCCGTAACAACCTCTCAAGCCT (SEQ ID NO: 75)	52
	Bg_5D	GAGCGTCCGTAACACCTCTCAAGCCTGAGCGTCCGTAACAACCTCTCAAGCCT (SEQ ID NO: 76)	54
<i>Bipolaris zeicola</i>	Bz-4D ^a	TTTCGGAGCGCAGCACATATTTGTTTCGGAGCGCAGCACATATTTG (SEQ ID NO: 77)	48
	Bz-5D ^a	CTGGGAGACTCGCCTTAAACGATTGCTGGGAGACTCGCCTTAAACGATTG (SEQ ID NO: 78)	52
	Bz-6D	GCTTGGTGTGGCGTTTTTGCTCCGCTTGGTGTGGCGTTTTGTCTCC (SEQ ID NO: 79)	54
	Bz-7D	CATTTTAACTTTGACCTCGGATCATTTAACCTTGACCTCGGAT (SEQ ID NO: 80)	48
<i>Colletotrichum cereale</i>	Cc_2D	CTACCAAGGGAGCTGGGCCCGCCGCTACCAGGGGACGTGGCCCGCCCG (SEQ ID NO: 81)	50
	Cc_3D	CCAGGGGACGTGGCGCCCGCCGGACAGGGGACGTGGCGCCGCCGGA (SEQ ID NO: 82)	48
	Cc_7D	ACGACGTTCTCTGAGTGGCACAAACGACGTTCTTGAGTGGCACA (SEQ ID NO: 83)	48
	Cc_9D	CTGAGTGGCACAAAGCAAATAATTCTGAGTGGCACAAAGCAAATAATT (SEQ ID NO: 84)	46
<i>Eudarluca caricis</i>	Ec_2D	CAGAAACCGCTTATACTCGGCAGAACCGCTCTATACTCGG (SEQ ID NO: 85)	42
	Ec_3D	GCCTGATTCTCCCCATGCTTGCCTGATTCTCCCCATGCTT (SEQ ID NO: 86)	42
	Ec_6D	ACGATAGCCTGAAGCGCAGCACATACGATAGCCTGAAGCGCAGCACAT (SEQ ID NO: 87)	48
	Ec_7D	CAGCGTCAGTAAAGTAATTAGCGTCAGTAACAAGTAATT (SEQ ID NO: 88)	42

TABLE 7-continued

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
<i>Puccinia coronata</i>	Pc_3D	AGAATAGAGTGCACCTTGATTGTGGCTAGAACAGAGTCACTTGATTGTGGCT (SEQ ID NO: 89)	52
	Pc_6D	TTATTAGGAGAGTTACATTACCCATTAGGAGAGTTACATTACCC (SEQ ID NO: 90)	46
	Pc_7D	CTTGGTTGCATGATTGAAAGAGTCACTTGGTTGCATGATTGAAAGAGTC (SEQ ID NO: 91)	48
	Pc_9D	TTAAAAAGACTTGTTGCATTAAAAGACTTGTTGCAT (SEQ ID NO: 92)	40
<i>Puccinia persistens</i> var <i>triticina</i>	Pp_t_1D	GCATTCTTATTGAATGTTCACAGCATTCTTATTGAATGTTACA (SEQ ID NO: 93)	48
	Pp_t_2D	CACTCTTGCATGATTGAAAGACACTTCTTGCATGATTGAAAGA (SEQ ID NO: 94)	48
	Pp_t_4D	AATCTTACCCAAACTTTAACACAACTTACCCAAACTTTAACAC (SEQ ID NO: 95)	46
	Pp_t_7D	GTTAGTGGATGTTGAGTGTGCTGTTAGTGGATGTTGAGTGTGCTGTC (SEQ ID NO: 96)	54
<i>Puccinia striiformis</i>	Ps_2D	ACGTAACCTCTTATTGAATGTTGACCGTAACCTCTTATTGAATGTTGC (SEQ ID NO: 97)	50
	Ps_7D	GTCACTTCTATAAGTGGATGTCACCTTCTATAAGTGGAT (SEQ ID NO: 98)	44
	Ps_9D	CATCTTATTAAAGGGAGACTCCATCTTATTAAAGGGAGACTC (SEQ ID NO: 99)	44
	Ps_10D	GAGACTCCTAAACACCAATGAGACTCCTAAACACCAAT (SEQ ID NO: 100)	40
<i>Puccinia graminis</i>	Pg_1D	ACTTTAAAAACTTGGTTGCATGAACCTTTAAAAACTTGGTTGCATGA (SEQ ID NO: 101)	48
	Pg_5D	TTAGTGGATGTTGAGTGTGCTGTACCTTAGTGGATGTTGAGTGTGCTGTAC (SEQ ID NO: 102)	54
	Pg_7D	CACTGCCATCTTGTGTTGTTACACTGCCATCTTGTGTTGTTA (SEQ ID NO: 103)	42
	Pg_8D	GAGTACGTAACATTCTTAATTGAGAGTACGTAACATTCTTAATTGA (SEQ ID NO: 104)	50
<i>Puccinia graminis f.</i> sp. <i>Triticici</i>	Pg_T1d	GCCATCTTTTGTAACAAAGAGACGCCATCTTTTGTAACAAGAGAC (SEQ ID NO: 105)	48
	Pg_T2d	CCCAATATCTATTTTTTAAGACCTCCAATATCTATTTTTTAAGACCT (SEQ ID NO: 106)	52
	Pg_T4d	AAACAGAGACTCTAAACACCAAAAGAGACTCCTAAACACCA (SEQ ID NO: 107)	44
	Pg_T3d	TGGGTTTTAGGAGTCTTGTGTTGGGTTTAGGAGTCTTGT (SEQ ID NO: 108)	44
<i>Pythium volutum</i>	Pv_2D	GTTCTGTGCCTCTCTTGGGAGGTTCTGTGCCTCTCTGGGAG (SEQ ID NO: 109)	44
	Pv_3D	GAAGGTTGGCTGCAAATGTAGTGAAGGTTGGCTGCAAATGTAGT (SEQ ID NO: 110)	48
	Pv_4D	CTGTATGCGCGGCTTCCGATGTACTGTATGCGCGGTCTCCGATGTA (SEQ ID NO: 111)	48
	Pv_10D	CTTGTGTTGAGAGAAGTGCTGACCCCTGTGTTGAGAGAAGTGCTGACC (SEQ ID NO: 112)	50
<i>Pythium torulosum/</i>	Pt_1D	GCGGTTTGCCGATGTAACCTTTAACGCGGTTTGCCGATGTACCTTAAAC (SEQ ID NO: 113)	52
	Pt_2D	GTACCTGCTTGTGAGGCAACGGTACCTGTCTGTGAGGCAACGG (SEQ ID NO: 114)	48
	Pt_3D	TGTCTGTGAGGCAACGGTCTGTCTGTGAGGCAACGGCTG (SEQ ID NO: 115)	48
	Pt_4D	GTACCTGCTTGTGAGGCAACGGTACCTGTCTGTGAGGCAACGG (SEQ ID NO: 116)	50
<i>Pythium arrhenomanes</i>	Parr_1D	TGTAATTTGTTTGTGCCTCTTCTGTAATTGTTGTGCCTCTTC (SEQ ID NO: 117)	52
	Parr_2D	GAAGGAAGGCACAAAACAAAATTACAGAAAGAAGGCACAAAACAAAATTACA (SEQ ID NO: 118)	52

TABLE 7-continued

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
<i>Pythium deliense</i>	Pd_1D	TACCTGATTGTGTGAGGCAATGGTTACCTGATTGTGTGAGGCAATGGT (SEQ ID NO: 119)	50
	Pd_2D	TCACTGTTCTGTGCCTCTCTCGGGATCATGTTCTGTGCTCTCTCGGAA (SEQ ID NO: 120)	50
	Pd_3D	CGTTGACTCCCTTTTCGGAGGAGAACGTTGACTCCCTTTCGGAGGAGAA (SEQ ID NO: 121)	50
	Pd_4D	GCTTAATTGTGGTCTGCCGATGTATTGCTTAATTGTGGTCTGCCGATGTATT (SEQ ID NO: 122)	54
<i>Pythium rostrativingens</i>	Pr_2D	GAGTCGGCTAACAGAAGGTGGGGAGTCGGCTAACAGAAGGTGG (SEQ ID NO: 123)	46
	Pr_5D	GACTCCGGTTTCTATTGCGTTGCTGACTCCGGTTTCTATTGCGTTGCT (SEQ ID NO: 124)	52
	Pr_6D	TTGGAGAAGGAGCAGAGGTGAAGTGGAGAAGGAGCAGAGGTGAAG (SEQ ID NO: 125)	44
	Pr_10D	CTCCAGAGCACGCTACCGAGGTCTCCAGAGCACGCTACCGAGGT (SEQ ID NO: 126)	44
<i>Pythium rostratum</i>	Prm_1D	GGACTGATGTGCGCTTGCGCATGTGGACTGATGTGCGCTTGCGCATGT (SEQ ID NO: 127)	50
	Prm_6D	TTAAACCATAACATAAGTACTGATTTAAACCATACCATAAAGTACTGATT (SEQ ID NO: 128)	50
	Prm_9D	TCTCCGCTGAGAGTTGTGTGTCTCCGCTGAGAGTTGTGT (SEQ ID NO: 129)	54
	Prm_10D	CTCTCCGCTGAGAGTTGTGTGTCTCCGCTGAGAGTTGTGT (SEQ ID NO: 130)	42
<i>Pyrhium aphanidermatum</i>	Pa_1D	GCTGCTTGGACGCCCTGTTTCGCTGCTCTGGACGCCCTGTTTC (SEQ ID NO: 131)	52
	Pa_2D	GCTGCTTGGACGCCCTGTTGCTGCTCTGGACGCCCTGTT (SEQ ID NO: 132)	42
	Pa_4D	GAECTTTGCAATTATTGTGAGACTGTTGCAATTATTGTGA (SEQ ID NO: 133)	44
	Pa_5D	GAAAGTTTATGGTTTAATCTAGAAAAGTTATGGTTTAATCTA (SEQ ID NO: 134)	44
<i>Pythium myriostylum</i>	Pm_1D	GATTAGAGATGGCAGAATGTGAGGTGGATTAGAGATGGCAGAATGTGAGGTG (SEQ ID NO: 135)	52
	Pm_2D	GCTCTGCGGAGGTGGCGACTTCGGTGCCTCGCGAGTGGCGACTTCGGT (SEQ ID NO: 136)	52
	Pm_4D	CCTGTCTTGTGTGGGCAATGGCTGCTGTCTTGTTGTTGGGCAATGGCTG (SEQ ID NO: 137)	52
	Pm_5D	CCTGTCTTGTGTGGGCAATGGCTGCTGTGTTGTTGGGCAATGGT (SEQ ID NO: 138)	46
<i>Pythium arrhenomanes</i>	Par_3D	GGTTGTCGCAGTGTAGTTAATTGGTTGTCGCCAAGTGTAGTTAATT (SEQ ID NO: 139)	50
	Par_5D	AGATGGCAGATGTGAGGTGTCTAGATGGCAGATGTGAGGTGTCT (SEQ ID NO: 140)	44
	Par_6D	GTGTCGTGAGAGAAGTGTGACCTGTGTCTGAGAGAAGTGTGACCT (SEQ ID NO: 141)	44
	Par_7D	AGTGGTTATTGCTTGGACGCAGTGGTTATTGCTTGGACGC (SEQ ID NO: 142)	44
<i>Rhizotonia solani</i>	Rs_2D	AACGAATGTAATTGATGTAACGAACGAATGTAATTGATGTAACG (SEQ ID NO: 143)	44
	Rs_4D	CTGGATCTCAGTGTATTGCTTGGCTGGATCTCAGTGTATTGCTTGG (SEQ ID NO: 144)	46
	Rs_5D	ACCCCTCTAATAGTCCATTGACACCGCTTCTAATAGTCCATTGAC (SEQ ID NO: 145)	46
	Rs_9D	GTAACGCATCTAATACTAAGTTGTAACGCATCTAATACTAAGTT (SEQ ID NO: 146)	46
<i>Ceratobasidium cereale</i>	Cr_4D	CCGTCCAATACAAAAATCTTACCGTCCAATACATAAAATCTTA (SEQ ID NO: 147)	44
	Cr_6D	TAATCAGAATGTAATCGATGTAACGTAATCAGAATGTAATCGATGTAACG (SEQ ID NO: 148)	52
	Cr_7D	GTAAACGCATCTATAAAACTAAGGTAACGCATCTATAAACTAAG (SEQ ID NO: 149)	44
	Cr_8D	GGCTTTGTTGGATTGGAGGTGGCTTTGTTGGATTGGAGGT (SEQ ID NO: 150)	48

TABLE 7-continued

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
<i>Waitea circinata</i>	Wc_1D	GTCCTCTGTAGACTCTGCTTCAGTCCCTGTAGACTCTGCTTC (SEQ ID NO: 151)	42
	Wc_2D	CTAGTGTCTAGTATGTGCACTAGTGTTCAGTATGTGCA (SEQ ID NO: 152)	42
	Wc_3D	GTAATAGATCTATGTGGATACGGTAATAGATCTATGTGGATACG (SEQ ID NO: 153)	44
	Wc_3D	TGAAGCAGAGTCTACAGGGACTGAAGCAGAGTCTACAGGGAC (SEQ ID NO: 154)	42
<i>Rhizoctonia zeae</i>	Wcz_1D	CCTCTGTAATAGATCTATGTGGATAACGCTCTGTAAATAGATCTATGTGGATAACG (SEQ ID NO: 155)	54
	Wcz_2D	CATGAATCTCTCAAATACAATGATTTCATGAATCTCTCAAATACAATGATT (SEQ ID NO: 156)	52
	Wcz_3D	CATGAATCTCTCAAATACAATGACATGAATCTCTCAAATACAATGA (SEQ ID NO: 157)	46
	Wcz_4D	CCTCTGTAATAGATCTATGTGCCTCTGTAAATAGATCTATGTG (SEQ ID NO: 158)	44
<i>Waitea circinata</i> var. <i>circinata</i>	Wcc_4D	TTATACACACACAATAGTCATTGTTACACACACAATAGTCATTG (SEQ ID NO: 159)	46
	Wcc_8D	CCTGTGCACCTTTGTAGTATTACCCGTGCACCTTTGTAGTATTAC (SEQ ID NO: 160)	48
	Wcc_11D	CAAATGTATTAGCTGGGGTTATATAGCAAATGTATTAGCTGGGGTTATATAG (SEQ ID NO: 161)	54
	Wcc_12D	TGGAGCTGTTGGCGAACATCGATGGAAGCTGTTGGCGCAAGTCGA (SEQ ID NO: 162)	50
<i>Rhizotonia oryzae</i>	Wco_1D	TATTTGAATCATTATTATGGACTATTTGAATCATTATTATGGAC (SEQ ID NO: 163)	50
	Wco_2D	CTTGGAAAGTTGTGCGCGCAAGCTTGGAAAGTTGTGCGCGCAAGT (SEQ ID NO: 164)	46
	Wco_3D	TGAGTGTATGAACTCTCAAATATGAGTGTATGAACTCTCAAATA (SEQ ID NO: 165)	48
	Wco_4D	ATTGGACTTGGAAAGTTGTGCGCATTTGGACTTGGAAAGTTGTGCGC (SEQ ID NO: 166)	48
	Wco_6D	TTGGAAAGTTGTGCGCGCAAGTTGGAAAGTTGTGCGCGCAAGT (SEQ ID NO: 167)	46
<i>Sclerotinia homoeocarpa</i>	Sh_1D	TCCAACCCTTGTTATCTTACCATCCAACCCTTGTTATCTTACCA (SEQ ID NO: 168)	48
	Sh_2D	CCTTGTGTATCTTACCATGTTCTTGTTATCTTACCATGTT (SEQ ID NO: 169)	44
	Sh_4D	ACAGCCTCAGCGCCCTCCGGGCCACAGCCTCAGCGCCCTCCGGGCC (SEQ ID NO: 170)	48
	Sh_5D	AGGAAAATCACAACCTGAAATTGAGGAAAATCACAACTCTGAATTG (SEQ ID NO: 171)	46
<i>Typhula incarnata</i>	Ta_2D	ATGGGGTTCTGCTTCAATCGTCATGGGTTCTGCTTCTAATCGTC (SEQ ID NO: 172)	46
	Ta_3D	CTCTTGTGTTGCGCAGACTATGCTCTTGTGGTGCAGACTATG (SEQ ID NO: 173)	44
	Ta_5D	GTGATAATTATCTACGCTGTGGTTGTATAATTATCTACGCTGTGGTT (SEQ ID NO: 174)	48
	Ta_6D	GCTCGGAATTAACTATGGGCTCGAATTAACTATGGG (SEQ ID NO: 175)	40
<i>Typhula ishikariensis</i>	Ti_2D	CTACGCTGTTGGCTTGAACTACGCTGTTGGCTTGAA (SEQ ID NO: 176)	42
	Ti_3D	GGTCTTGTGAAGCACTTTATGTGGCTTGTTGTGAAGCACTTATTGT (SEQ ID NO: 177)	46
	Ti_4D	GTTACGAGGTTCTGCTTCTAATCGTTACGAGGTTCTGCTTCTAATC (SEQ ID NO: 178)	46
	Ti_5D	TTCTAATCGTCCTTACTGCTTCTAATCGTCCTTACTG (SEQ ID NO: 179)	40
<i>Gaeumannomyces graminis</i>	Gg_1D	CTGTTGCTCGGGGGACGATGGCTGTTGCTTCGGCGGACGATGG (SEQ ID NO: 180)	44
	Gg_2D	GACGCCGCGGGAGGTTACAAACCGACGCCGCCGGAGGTTACAAACC (SEQ ID NO: 181)	46
	Gg_3D	GGACGCCGCCGGAGGTTACAGGACGCCGCCGGAGGTTACA (SEQ ID NO: 182)	40
	Gg_4D	CGGCCCGGCCGGTGGGGCCCCACGCCGCCGGAGGTTACCA (SEQ ID NO: 183)	42

TABLE 7-continued

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
<i>Magnaporthe grisea</i>	Mg_1D	CAACCCCTCAAGCCCCGGCTTGGTCAACCCTCAAGCCCCGGCTTGGT (SEQ ID NO: 184)	46
	Mg_2D	GCACTCTGAGCCTAAAGACAAGCATCTCTGAGCCTAAAGACAA (SEQ ID NO: 185)	46
	Mg_5D	GAACCCCTCGCTCGGCCCGTCACCGAACCCCTCGCTCGGCCCGTCACC (SEQ ID NO: 186)	46
<i>Magnaporthe oryzae</i>	Mo_1D	GCCTCGGCTTGGTGTGGGCGCCTCGGCTTGGTTGGGTC (SEQ ID NO: 187)	42
	Mo_5D	CACGCCCGCCGGAGGTTCAAAACTCACGCCGCCGGAGGTTCAAAACT (SEQ ID NO: 188)	48
	Mo_6D	CGCCGGAGGTTCAAAACTCTTATTGCGCCGGAGGTTCAAAACTCTTATT (SEQ ID NO: 189)	40
	Mo_10D	GTGCTCCAGCCGCTAAACCCCCAATTGCGCTCCAGCCGCTAAACCCCCAATTC (SEQ ID NO: 190)	50
<i>Magnaporthe poae</i>	Mp_1D	CGCCGCCGGAGGTTCAAAACCCGCCGCCGGAGGTTCAAAACC (SEQ ID NO: 191)	42
	Mp_2D	CCGCCGGAGGTTCAAAACCCCTCCGCCGGAGGTTCAAAACCCCT (SEQ ID NO: 192)	42
	Mp_3D	AACCGGCCCTCGCTCGGCCGGAACCGGCCCTCGCTCGGCCGC (SEQ ID NO: 193)	42
<i>Gaeumannomyces incrustans</i>	Gi_1D	GCTCCGAGCGCAGTAGCACGCGCTCCGAGCGCAGTAGCACGC (SEQ ID NO: 194)	42
	Gi_2D	GGTTGGCGCCGGTGCCCAGATGGGTTGGCGCCGGTGCCCAGATG (SEQ ID NO: 195)	44
	Gi_3D	GTCGCCGCCGGAGGTTCGAAACCGTCGCCGCCGGAGGTTCGAAACCC (SEQ ID NO: 196)	46
	Gi_4D	CCGCCGGAGGTTCGAAACCCCTCCGCCGGAGGTTCGAAACCCCT (SEQ ID NO: 197)	42
<i>Magnaporthe rhizophila</i>	Mr_1D	TTCGAAACCTGAATTCTAGTGTTCGAAACCCCTGAATTCTAGTG (SEQ ID NO: 198)	44
	Mr_2D	GAGGTCGCCGCCGGAGGTTCGAAGAGGTCGCCGCCGGAGGTTCGAA (SEQ ID NO: 200)	46
	Mr_3D	GCCTGGAGGTCGCCGCCGGAGGTTCGCCTGGAGGTCGCCGCCGGAGGTT (SEQ ID NO: 201)	50
	Mr_4D	CCAGATGGGCTGGAGGTCGCCGCCAGATGGGCTGGAGGTCGCCGC (SEQ ID NO: 202)	48
<i>Magnaporthe salvinii</i>	Ms_1D	AAAGTACATCGGCCGGACCCGCTGGGAAGTACATCGGCCGGACCCGCTGGG (SEQ ID NO: 203)	48
	Ms_2D	GGCGGACCCGCTGGGGCCCTGAGGGCGGACCCGCTGGGCCCTGAG (SEQ ID NO: 204)	46
	Ms_3D	CGCTTCGCTCGGTGAGATCCC GGAGGCGCCTCGCTCGGTGGATCCCCGGAGG (SEQ ID NO: 205)	52
	Ms_4D	CCGGAGGGCATTCCAGCCGCTAACCGGAGGGCATTCCAGCCGCTAAA (SEQ ID NO: 206)	48
<i>Microdochium bolleyi</i>	Mb_1D	CTGGAAACAGTGTGCCACCGGTGGACTGGAAACAGTGTGCCACCGGTGGA (SEQ ID NO: 207)	46
	Mb_4D	AAGCCGGCCAGACGACAGCCATAAAAGCCGGCAGACGACAGCCATAAA (SEQ ID NO: 208)	48
	Mb_5D	GCCAGACGACAGCCATAAAACCGCCAGACGACAGCCATAAAACC (SEQ ID NO: 209)	42
	Mb_6D	CTGGAAACAGTGTGCCACCGGTCTGGAAACAGTGTGCCACCGGT (SEQ ID NO: 210)	46
<i>Microdochium nivale</i>	Mn_2D	GGTGGATGGTGCTGTCTCGGGTGGATGGTGCTGTCTCG (SEQ ID NO: 211)	42
	Mn_4D	TGGACTACCTAAACTCTGTTATGGACTACCTAAACTCTGTTA (SEQ ID NO: 212)	42
	Mn_5D	GTCAATCTGAATCAAACTAAGGTCAATCTGAATCAAACAA (SEQ ID NO: 213)	42
	Mn_9D	CGGAGTCGGTTCGTGTCTGACGGAGTCGGTTCGTGTCTGA (SEQ ID NO: 214)	42

TABLE 7-continued

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
<i>Gleocercospora sorghi</i>	Gs_1D	CTCGGTGGTTAGTACTCTCTCGCTCGGTGGTTAGTACTCTCTCTCG (SEQ ID NO: 215)	48
	Gs_2D	CGGTGGTTAGTGCCTCTCTCGGCGGTGGTTAGTGCCTCTCTCGG (SEQ ID NO: 216)	46
	Gs_4D	TCTCTCTCGGGAGGGTGCCTGCCTCTCGGGAGGGTGCCTGC (SEQ ID NO: 217)	44
	Gs_6D	GTAAATTACTTATCTCGCTTGTAAATTACTTATCTCGCTTCTT (SEQ ID NO: 218)	44
<i>Laetisaria fuciformis</i>	Lf_1D	CCTTGGGTGTCGAGTTGATTCCCTTGGGTGTCGAGTTGATT (SEQ ID NO: 219)	46
	Lf_2D	TTTCCGCGCTGGACTGTGTAAATTCCGCGCTGGACTGTGTAAA (SEQ ID NO: 220)	44
	Lf_3D	CGCGTTGTATGAGACTCAGCCTCGCGTTGTATGAGACTCAGCCT (SEQ ID NO: 221)	44
	Lf_5D	GGCATCCTTGGGTGTCGAGTTGGGCATCCTTGGGTGTCGAGTTG (SEQ ID NO: 222)	48
<i>Leptosphaeria korrae</i>	Lk_1D	TAAAGCAATTGGCAGCCTATATCTTAAAGCAATTGGCAGCCTATATCT (SEQ ID NO: 223)	48
	Lk_2D	AGCACAAACTGCATGGCGGAGCACAAACTGCATGGCGG (SEQ ID NO: 224)	40
	Lk_3D	CCCATGAAACCTATTATTTCCCATTGAACCTATTATTT (SEQ ID NO: 225)	42
	Lk_6D	AGCAATTGGCAGCCTATATCTGGAGCAATTGGCAGCCTATATCTGG (SEQ ID NO: 226)	46
<i>Ophiostphaerella herpotricha</i>	Oh_1D	TCTTACTGCCAGTTATAGGCACTCTTACTGCCAGTTATAGGCAC (SEQ ID NO: 227)	48
	Oh_2D	GTGTAGAACAAACTACGCAGACGTGAGAACAAACTACGCAGAC (SEQ ID NO: 228)	44
	Oh_3D	CCAATAAGCCTTTTATCACCCATAAGCCTTTATCAC (SEQ ID NO: 229)	40
	Oh_4D	TCTACTCCACTGCCCTTGGACTCGTCACTCCACTCGCTTGGACTCG (SEQ ID NO: 230)	48
<i>Ophiostphaerella agrostis</i>	Oa_1D	AGAACATAGGCCCAAGCTGTAGCAGAACATAGGCCCAAGCTGTAGC (SEQ ID NO: 231)	48
	Oa_4D	AAGGCCTCTCTATACCCCTGTAAGGCCTCTCTATTACCCCTGT (SEQ ID NO: 232)	46
	Oa_5D	ATCATACATTAGAACATAGGCCATCATTACATTAGAACATAGGCC (SEQ ID NO: 233)	46
	Oa_11D	GGTGTTCCTCCATTGCGGGTGTCTCCATTGCG (SEQ ID NO: 234)	46
<i>Limonomyces roseipellis</i>	Lr_1D	ATATCAATAACACAAACTAACAGATATCAATAACACAAACTAACAG (SEQ ID NO: 235)	48
	Lr_2D	CTGGCATCCTCCGGGTGTCGAGCTGGCATCCTCCGGGTGTCGAGT (SEQ ID NO: 236)	48
	Lr_3D	CTTGTAGTTGTGTTATTGATATCTTGTAGTTGTGTTATTGATAT (SEQ ID NO: 237)	48
	Lr_4D	ACTCGGACACCCGGAGGATGCCAGACTCGGACACCCGGAGGATGCCAG (SEQ ID NO: 238)	48
<i>Acidovorax avenae</i>	Aa_1D	ATAAAGGGAGGTCACTGACGGTATAAGGGAGGTCACTGACGGT (SEQ ID NO: 239)	42
	Aa_2D	CTAATAAAGGGAGGTCACTGACGCTATAAAGGGAGGTCACTGACG (SEQ ID NO: 240)	44
	Aa_3D	CGTCATGACCTCCCTTATTAGCGTCATGACCTCCCTTATTAG (SEQ ID NO: 241)	44
	Aa_4D	ACCGTCATGACCTCCCTTATACCGTCATGACCTCCCTTAT (SEQ ID NO: 242)	42
<i>Xanthomonas translucens</i> pv. <i>poae</i>	Xt-p_1D	AGTGAAATGCGTAAGATCGGGAGGAAGTGAAATGCGTAAGATCGGGAGGA (SEQ ID NO: 243)	50
	Xt-p_2D	CACCGAACTTCCAGAGATGGATTGCA CGGA ACTTCCAGAGATGGATTG (SEQ ID NO: 244)	50
	Xt-p_3D	CACAGTGGTAGCAATACCATGGGTGCA CGACAGTGGTAGCAATACCATGGGT (SEQ ID NO: 245)	50
	Xt-p_4D	CACAGTGGTAGCAATACCATGCA CGACAGTGGTAGCAATACCATG (SEQ ID NO: 246)	42

TABLE 7-continued

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
<i>Curvularia trifolii</i>	ct_1	GGCGTCTTGTCTTGCGCTCTGGCGTCTTGTCTTTGGCTCT (SEQ ID NO: 247)	44
	ct_2	GGCTTTGCCAAAGACTCGGCTCTTGCCCAAAGACTC (SEQ ID NO: 248)	40
	ct_3	CGCAGGACCAACCCATAAACCTGCCAGGACCACACCATAAACCT (SEQ ID NO: 249)	46
	ct_4	GCGCCAGGACCAACCCATAAGCCGCCAGGACCACACCATAA (SEQ ID NO: 250)	42
<i>Trichoderma virens</i>	tv_1	C GTTACCAAACTGTTGCCTCGGCCGTTACCAAAC TGTGCCTCGC (SEQ ID NO: 251)	46
	tv_4	CAACCCCTCGAACCCCTCCGGCAACCCCTCGAACCCCTCCGG (SEQ ID NO: 252)	42
	tv_5	GTATTCTGGCGGGCATGCCTGTCCGTATTCTGGCGGGCATGCCTGTCC (SEQ ID NO: 253)	48
<i>Urocystis agropyri</i>	Ua_1	GATCTGTATCCGCCCCCGACCCGATCTGTATCCGCCCCGACCC (SEQ ID NO: 254)	44
	Ua_3	GTATCCGCCCCGACCCCTTCGATCGTATCCGCCCCGACCCCTTCGATC (SEQ ID NO: 255)	48
	Ua_4	GAGGGTAGCGCCGTTCATGGTCGGAGGGTAGCGCCGTTCATGGTC (SEQ ID NO: 256)	48
	Ua_5	CTAATCTAGGAGTGGCATCGA ACTAATCTAGGAGTGGCATCGAA (SEQ ID NO: 257)	44
	Us_1	CGCCC ATATCGAGTTTGCTCGCGCCATATCGAGTTTGCTCG (SEQ ID NO: 258)	48
<i>Ustilago striiformis</i>	Us_2	TTACAATGAAATCGACTGGTAATGCTTACAATGAAATCGACTGGTAATGC (SEQ ID NO: 259)	50
	Us_3	ACAATGAAATCGACTGGTAATGCACAATGAAATCGACTGGTAATGC (SEQ ID NO: 260)	46
	Ly_1	GCACACTTGTCTTGACTTTATT CGCACACTTGCTTGACTTTATTC (SEQ ID NO: 261)	46
<i>Lycoperdon spp</i>	Ly_4	GGAGCATGTGCACACTTGCTTGAGCATGTGCACACTTGCTT (SEQ ID NO: 262)	44
	Ly_5	CGAGTTGTGATGGGCTTGGATCCGAGTTGTGATGGGCTTGGATC (SEQ ID NO: 263)	46
	Bov_1	TCCGGATGTGAGGAATTGCTGAGTTCCGGATGTGAGGAATTGCTGAGT (SEQ ID NO: 264)	48
<i>Bovista</i>	Bov_2	TACCTCTCCTCAAGTACTATGTTACCTCTCCTCAAGTACTATGT (SEQ ID NO: 265)	46
	Bov_4	ATTAATTCTCAACCCCTCTAGCTTATTAAATTCTCAACCCCTCTAGCTT (SEQ ID NO: 266)	52
	Bov_6	AAATTCTCAACCCCTCTAGCTTAAATTCTCAACCCCTCTAGCTT (SEQ ID NO: 267)	44
	Ag_1	TGGACTTCATTTCATCCACCTGTGGACTTCATTTCATCCACCTG (SEQ ID NO: 268)	46
<i>Agaricus</i>	Ag_6	TCTTTCTCTGTTAGAGTCTATGTTCTTTCTGTTAGAGTCTATGT (SEQ ID NO: 269)	48
	Ag_7	TTGAGCTTTCTAGGTTATGTTGAGCTTTCAAGGTATTG (SEQ ID NO: 270)	44
	Ag_8	GTTGAAAGGAGAGCTGGATTGTTGAAAGGAGAGCTGGATTGT (SEQ ID NO: 271)	48
	Mar_1	TTGGTATTCCGAGAGGCATGCCCTGGTATTCCGAGAGGCATGCC (SEQ ID NO: 272)	48
<i>Marasmius</i>	Mar_2	TTGCCCTCTGGTATTCCGAGAGGTTGCCCTGGTATTCCGAGAGG (SEQ ID NO: 273)	50
	Le_1	CATGAGTATGTTGCCAGAATGCATGTAGTATGTTGCCAGAATG (SEQ ID NO: 274)	44
<i>Lepiota</i>	Le_2	ACCATGAGTATGTTGCCAGAATGACCATGTAGTATGTTGCCAGAATG (SEQ ID NO: 275)	48
	Le_3	TATCACAAACCATGTAGTATGTTATCACAAACCATGTAGTATGTT (SEQ ID NO: 276)	46

TABLE 7-continued

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
<i>Athelia rolfsii</i>	At_2	ACATAGAACGATCTCATATTGAAACATAGAACGATCTCATATTGAA (SEQ ID NO: 277)	46
	At_3	ACTCTTATTGTATGTTACATAGAACACTCTTATTGTATGTTACATAGAAC (SEQ ID NO: 278)	50
	At_6	AGACTCATTAAATTCTCAACCTTAGAGTCATTAAATTCTCAACCTT (SEQ ID NO: 279)	46
	At_7	CAAGGCTTGGATGTGAGAGTTGCTCAAGGCTTGGATGTGAGAGTTGCT (SEQ ID NO: 280)	48
<i>Gibberella zaeae</i>	Gz_3	AAGGGACGGCCCGCCGCAGGAACCCAAGGGACGGCCCGCCGCAGGAACCC (SEQ ID NO: 281)	50
	Gz_5	CTGCACTCCCCAATACATTGGCGCTGCACTCCCCAATACATTGGCG (SEQ ID NO: 282)	48
	Gz_6	GCTGCACTCCCCAATACATTGGCGCTGCACTCCCCAATACATTGGC (SEQ ID NO: 283)	48
<i>Fusarium oxysporum</i>	Poxy_3	GGACTCGCGTTAACCGCGTCCGGACTCGCGTTAACCGCGTTCC (SEQ ID NO: 284)	46
	Poxy_4	CGCTTCCCTCAAATTGATTGGCGGTGCGTTCCCTCAAATTGATTGGCGGT (SEQ ID NO: 285)	50
	Po1R	CGTTCCCTCAAATTGATTGGCGGTGCGTTCCCTCAAATTGATTGGCGTC (SEQ ID NO: 42)	48
	Pox2R	GTTGGGACTCGCGTTAACCGCGTCCGGACTCGCGTTAACCG (SEQ ID NO: 43)	42
<i>Fusarium spp</i>	Fus_1	TGTTGCCCTCGGCGGATCAGCCCGCTGTTGCCCTCGGCGATCAGCCCGC (SEQ ID NO: 286)	48
	Fus_2	AAATAAATCAAAACTTCAACAAAAATAATCAAAACTTTCAACAA (SEQ ID NO: 287)	46
<i>Poa annua</i> (RBCL)	Poa_R_1	CCTCAGCCTGGAGTTCCCCCGGACCTCAGCCTGGAGTTCCCCCGGA (SEQ ID NO: 288)	46
	Poa_R_2	ACATTGAGCCTGTTGCTGGGGAAAGATAACATTGAGCCTGTTGCTGGGGAAAGAT (SEQ ID NO: 289)	52
	Poa_R_4	CTCAGCCTGGAGTTCCCCCGGACTCAGCCTGGAGTTCCCCCGGA (SEQ ID NO: 290)	44
<i>Lolium perenne</i> (RBCL)	Lp_R_1	CATATCGAGCCTGTTGCTGGGGAAAGACATATCGAGCCTGTTGCTGGGGAAAGA (SEQ ID NO: 291)	52
	Lp_R_3	TATCGAGCCTGTTGCTGGGGAAAGACATATCGAGCCTGTTGCTGGGGAAAGACA (SEQ ID NO: 292)	52
<i>Agrostis stolonifera</i> (RBCL)	As_R_1	AGTCCTCAACCTGGGGTCCGCCGAGTCCTCAAACCTGGGGTCCGCCG (SEQ ID NO: 293)	48
	As_R_2	AGTCCTCAACCTGGGGTCCGCCGAGTCCTCAAACCTGGGGTCCGCCGGA (SEQ ID NO: 294)	52
<i>Poa annua</i> (matK)	Poa_m_3	CGAGTAAGATGGAACATTGGCGAGTAAGATGGAACATTGG (SEQ ID NO: 295)	44
<i>Poa pratensis</i> (matK)	Pop_m_1	TGCCAAAATTGCGATACCATAGTTCTGCCAAATTGCGATACCATAGTTC (SEQ ID NO: 296)	48
	Pop_m_2	GAATGCCAAAATTGCGATACCATAGTGAATGCCAAATTGCGATACCATAGT (SEQ ID NO: 297)	50
<i>Agrostis stolonifera</i> (matK)	As_m_1	CTATCCATTGGAAATCTGGTGACTATCCATTGAAATCTGGTGCA (SEQ ID NO: 298)	50
	As_m_2	GCAACTCTTCAATACCGTATCAAGCAACTCTTCAATACCGTATCAA (SEQ ID NO: 299)	48
	As_m_4	ATTATCTCTGGAACTTTCTGGAAATTATCTCTGGAACTTTCTGG (SEQ ID NO: 300)	48
	As_m_5	TGCAACTCTTCAATACCGTATCAATGCAACTCTTCAATACCGTATCAA (SEQ ID NO: 301)	50
Positive control	ITS2R	GCTCGGTTCTTCATCGATGCGCTGCGTTCTTCATCGATGC (SEQ ID NO: 48)	40
Negative control ^b	ITS2_2_IR	GCTCGGTTGATCATCGATGCGCTGCGTTGATCATCGATGC (SEQ ID NO: 57)	40
Positive control	ITS4R	TCCCTCGCTTATTGATATGCTCCTCCGCTTATTGATATGC (SEQ ID NO: 49)	40
Negative control	ITS4_2_1R	TCCCTCGTTATTGATTTGCTCCTCCGTTATTGATTTG (SEQ ID NO: 302)	40
Negative control	ITS4_2_2R	TCCCTCGTTATTGAAATGCTCCTCCGTTATTGAAATGC (SEQ ID NO: 303)	40

TABLE 7-continued

Additional dimeric oligonucleotide probes			
Pathogen (Probe Target)	Probe Name	Probe Sequence	Probe Length
Negative control	ITS4_2_3R	TCCTCCGTTATTGGTATGCTCCTCGTTATTGGTATGC (SEQ ID NO: 304)	40
Positive control	matK-390F	CGATCTATTCAATTTCGATCTATTCAATATTTC (SEQ ID NO: 305)	44
Positive control	matK-1326R	TCTAGCACACGAAAGTCGAAGTTCTAGCACACGAAAGTCGAAGT (SEQ ID NO: 306)	44
Positive control	rbcLaF	ATGTCACCACAAACAGAGACTAAAGCATGTCACCACAAACAGAGACTAAAGC (SEQ ID NO: 307)	52
Positive control	rbcL-1F	ATGTCACCACAAACAGAAACATGTCACCACAAACAGAAAC (SEQ ID NO: 308)	40

Negative control probe sequences contain nucleotide mismatches as compared to the corresponding positive control probe sequence; these nucleotides are shown in bold.

All documents cited herein are incorporated by reference. While certain embodiments of invention are described, and many details have been set forth for purposes of illustration, certain of the details can be varied without departing from the basic principles of the invention.

The use of the terms "a" and "an" and "the" and similar terms in the context of describing embodiments of invention are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The terms "comprising," "having," "including," and "containing" are to be construed as open-ended terms (i.e., meaning "including, but not limited to") unless otherwise noted. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individu-

ally to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. In addition to the order detailed herein, the methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to better illuminate embodiments of invention and does not necessarily impose a limitation on the scope of the invention unless otherwise specifically recited in the claims. No language in the specification should be construed as indicating that any non-claimed element is essential to the practice of the invention.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 308

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<210> SEQ ID NO 2
<211> LENGTH: 24
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 2

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<210> SEQ ID NO 3
<211> LENGTH: 24
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gaggtgtacc tgaatttgtt gagg

24

<210> SEQ ID NO 4
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 4

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46

<210> SEQ ID NO 5
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 5

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48

<210> SEQ ID NO 6
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 6

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48

<210> SEQ ID NO 7
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 7

ggagagagat ggcagaatgt gagaaaaaaaaaa aaaggagaga gatggcagaa tgttag

56

<210> SEQ ID NO 8
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 8

gggagagaga tggcagaatg tgagaaaaaaaaaa aaaaggagaga gagatggcag aatgttag

58

<210> SEQ ID NO 9
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 9
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<211> LENGTH: 34
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 11
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<210> SEQ ID NO 12
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<220> FEATURE:
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<400> SEQUENCE: 13
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 14
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<210> SEQ ID NO 15
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 15

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 16

cagtgttatg ctgggttcca ctc 23

<210> SEQ ID NO 17
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 17

tgttgaaact tagtattttaga tgcgt 25

<210> SEQ ID NO 18
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 18

gagtggaaacc aagcataaca ctg 23

<210> SEQ ID NO 19
<211> LENGTH: 46
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 19

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<210> SEQ ID NO 20
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 20

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<210> SEQ ID NO 21
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 21

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<210> SEQ ID NO 22
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 22

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<210> SEQ ID NO 23
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 23

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<210> SEQ ID NO 24
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 24

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<210> SEQ ID NO 25
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 25

tccgcgtatgtt gctaacacctt cgc 23

<210> SEQ ID NO 26
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 26

cctgtgaaca tacctaaacgtt 23

<210> SEQ ID NO 27
<211> LENGTH: 24
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 27

ttatacaact catcaaccctt gtga 24

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<210> SEQ ID NO 28
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tcgcgttagta gctaaccacct cgctcgctga gtagctaaca cctcgc 46

<210> SEQ ID NO 29
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 29

cctgtgaaca tacctaaacg ttgcctgtga acatacaccaa acgttg 46

<210> SEQ ID NO 30
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 30

ttataacaact catcaaccct gtgattatac aactcatcaa ccctgtga 48

<210> SEQ ID NO 31
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 31

tcgcgttagta gctaaccacct cgcaaaaaaa aaatcgctga gtagctaaca cctcgc 56

<210> SEQ ID NO 32
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 32

cctgtgaaca tacctaaacg ttgaaaaaaaaaa aaacctgtga acatacaccaa acgttg 56

<210> SEQ ID NO 33
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 33

ttataacaact catcaaccct gtgaaaaaaaaaa aaaattatac aactcatcaa ccctgtga 58

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<210> SEQ ID NO 34
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 34

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33

<210> SEQ ID NO 35
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 35

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33

<210> SEQ ID NO 36
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 36

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34

<210> SEQ ID NO 37
<211> LENGTH: 43
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 37

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43

<210> SEQ ID NO 38
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 38

cctgtgaaca tacctaaacg ttgaaaaaaaaaaa aaaaaaaaaaaaaaaa aaa

43

<210> SEQ ID NO 39
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 39

ttatacaact catcaaccct gtgaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaa

44

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<210> SEQ ID NO 40
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 40

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24

<210> SEQ ID NO 41
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 41

gttgggactc gcgttaattc g

21

<210> SEQ ID NO 42
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 42

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48

<210> SEQ ID NO 43
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 43

gttgggactc gcgttaattc ggttggact cgcgtaattt cg

42

<210> SEQ ID NO 44
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 44

cgttcctcaa attgattggc ggtcaaaaaaa aaaacgttcc tcaaatttat tggcggtc

58

<210> SEQ ID NO 45
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 45

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52

<210> SEQ ID NO 46

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 46

gctgcgttct tcatcgatgc 20

<210> SEQ ID NO 47
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 47

tccctccgctt attgatatgc 20

<210> SEQ ID NO 48
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 48

gctgcgttct tcatecgatgc gctgcgttct tcatcgatgc 40

<210> SEQ ID NO 49
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 49

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<210> SEQ ID NO 50
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 50

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<210> SEQ ID NO 51
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<210> SEQ ID NO 52
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 52

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30

<210> SEQ ID NO 53
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 53

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30

<210> SEQ ID NO 54
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 54

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40

<210> SEQ ID NO 55
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 55

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<210> SEQ ID NO 56
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 56

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20

<210> SEQ ID NO 57
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 57

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<210> SEQ ID NO 58
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<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 58

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<210> SEQ ID NO 59
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 59

gctgcgttga tcatcgatgc aaaaaaaaaa 30

<210> SEQ ID NO 60
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 60

gctgcgttga tcatcgatgc aaaaaaaaaa aaaaaaaaaa 40

<210> SEQ ID NO 61
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Pythium torulosum

<400> SEQUENCE: 61

ggagagaaat ggcagaatgt gag 23

<210> SEQ ID NO 62
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Pythium volutum

<400> SEQUENCE: 62

ggagagaaat ggcagatgt ag 22

<210> SEQ ID NO 63
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Pythium torulosum

<400> SEQUENCE: 63

aggagagaaa tggcagaatg tgag 24

<210> SEQ ID NO 64
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Pythium volutum

<400> SEQUENCE: 64

aggagagaaa tggcagatgt gag 23

<210> SEQ ID NO 65
<211> LENGTH: 24
<212> TYPE: DNA

<213> ORGANISM: Pythium sp.

<400> SEQUENCE: 65

gaggtgtacc tgtcttgtt gagg

24

<210> SEQ ID NO 66

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Fusarium equiseti

<400> SEQUENCE: 66

tagcgttagta gctaacaacctt cgt

23

<210> SEQ ID NO 67

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Fusarium solani

<400> SEQUENCE: 67

cctgtgaaca tacctaaaac gttt

24

<210> SEQ ID NO 68

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Fusarium equiseti

<400> SEQUENCE: 68

cctgtgaaca tacctacgtt g

21

<210> SEQ ID NO 69

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Fusarium solani

<400> SEQUENCE: 69

ttattcaact catcaaccctt gtta

24

<210> SEQ ID NO 70

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Fusarium sp.

<400> SEQUENCE: 70

ttataacaact catcaaaccctt ctgtta

26

<210> SEQ ID NO 71

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Fusarium equiseti

<400> SEQUENCE: 71

cggtccctcaa atcgattgggg ggtc

24

<210> SEQ ID NO 72

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Fusarium equiseti

<400> SEQUENCE: 72

gttggggactc gcggtaaccctt g

21

<210> SEQ ID NO 73

<211> LENGTH: 44

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 73

tgtaactctc cgcgttagtaa tatgtaactc tccgcgtagt aata

44

<210> SEQ ID NO 74
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 74

gttgaccctc caccctgttc gattagttga ccctccaccc gtgtcgat

50

<210> SEQ ID NO 75
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 75

agcgtccgta acaacctctc aaggcttagcg tccgtaacaa cctctaagc ct

52

<210> SEQ ID NO 76
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 76

gagcgtccgtaacaacctctc caaggcttagcg cgccgtaacaa acacctctcaa gcct

54

<210> SEQ ID NO 77
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 77

tttcggagcg cagcacatat tttgtttcg agcgacgac atattttgc

48

<210> SEQ ID NO 78
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 78

ctggggagact cgccctaaaaa cgattgctgg gagactcgcc ttaaaacgtat tg

52

<210> SEQ ID NO 79
<211> LENGTH: 54
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 79

gcttgggtttt gggcgaaaaa tgtctccgt tggtgttggg cgtttttgtt ctcc 54

<210> SEQ ID NO 80
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 80

catttttaac ttttgacacc ggatcatttt taacttttga cctcgat 48

<210> SEQ ID NO 81
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 81

ctaccagggg acgtggcgcc cgccgcgtacc aggggacgtg gcccggccg 50

<210> SEQ ID NO 82
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 82

ccaggggacg tggcgccccgc cggaccaggg gacgtggcgcc ccggccgga 48

<210> SEQ ID NO 83
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 83

acgacgtttc ttctgagtgg cacaacgacg tttcttctga gtggcaca 48

<210> SEQ ID NO 84
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 84

ctgagtggca caagcaaata attctgagtgc gcacaagcaa ataatt 46

<210> SEQ ID NO 85
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 85

cagaaaaccgc tctatactcg gcagaaaaccg ctctatactc gg 42

<210> SEQ ID NO 86
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 86

gcctgattct ccccatgtct tgccctgattc tccccatgtc tt 42

<210> SEQ ID NO 87
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 87

acgatagcct gaagcgcgc acatacgata gcctgaagcg cagcacat 48

<210> SEQ ID NO 88
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 88

cagcgtcagt aacaagtaat tcagcgtcag taacaagtaa tt 42

<210> SEQ ID NO 89
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 89

agaatagagt gcacttgatt gtggctagaa tagagtgcac ttgattgtgg ct 52

<210> SEQ ID NO 90
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 90

ttattaggag agttacatta cccttattag gagagttaca ttaccc 46

<210> SEQ ID NO 91
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 91

cttggttgca tgatttggaaa gagtcacttg gttgcgtatgt ttgaaagagt ca 52

<210> SEQ ID NO 92

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 92

ttaaaaaagac ttgggttgcata ttaaaaaagac ttgggttgcata 40

<210> SEQ ID NO 93

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 93

gcattcttta ttgaatgttc acagcattct ttattgaatgt ttcaca 46

<210> SEQ ID NO 94

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 94

cacttcttg catgatttga aagacacttc tttgcgtatgt ttgaaaga 48

<210> SEQ ID NO 95

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 95

aatcttaccc aaacttttaa cacaatctta cccaaacttt taacac 46

<210> SEQ ID NO 96

<211> LENGTH: 54

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 96

gttttagtggaa tgtttagtgt tgctgtcggt tagtggatgt tgagtgttgc tgtc 54

<210> SEQ ID NO 97

<211> LENGTH: 50

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 97

acgttaacttc tttattgaat gttgcacgta acttcttat tgaatgttgc 50

<210> SEQ ID NO 98

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 98

gtcactttc tataagttgg atgtcacttt tctataagtt ggat 44

<210> SEQ ID NO 99

<211> LENGTH: 42

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 99

catcttattt aaggagact ccatcttatt taagggagac tc 42

<210> SEQ ID NO 100

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 100

gagactccta aaaacccaat gagactccta aaaacccaat 40

<210> SEQ ID NO 101

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 101

actttaaaaa acttggttgc atgaactttt aaaaacttgg ttgcatga 48

<210> SEQ ID NO 102

<211> LENGTH: 54

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 102

ttagtggatg ttgagtgttg ctgtacctta gtggatgttg agtgttgctg tacc 54

<210> SEQ ID NO 103

<211> LENGTH: 42

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 103

cacttgcacat cttgtttgtt acacttgcca tcttgtttgt ta 42

<210> SEQ ID NO 104
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 104

gagttatacgta aacattctta attgagagta tacgtaacat tcttaattga 50

<210> SEQ ID NO 105
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 105

gccccatctttt ttgttaacaag agacgccatc tttttgtaa caagagac 48

<210> SEQ ID NO 106
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 106

cccaaatatct atttttttta agacctccca atatctatTT ttttaagac ct 52

<210> SEQ ID NO 107
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 107

aacaaagagac tcctaaaacc caaacaagag actcctaaaa ccca 44

<210> SEQ ID NO 108
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 108

tgggttttag gagtccttgc ttgggtttt aggagtctct tgtt 44

<210> SEQ ID NO 109
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 109

gttctgtgcc ttctttggg aggttctgtg ctttccttg ggag

44

<210> SEQ ID NO 110
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 110

gaagggttgc tgcaaatgta gtgaaggttg gctgcaaatg tagt

44

<210> SEQ ID NO 111
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 111

ctgttatgcgc ggtcttccga tgtactgtat gcgcggtctt ccgatgtat

48

<210> SEQ ID NO 112
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 112

cttgttgc agagaagtgc tgacccttgt gttttagaga agtgctgacc

50

<210> SEQ ID NO 113
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 113

gcgggtttgc cgatgtactt ttaaacgcgg ttttgcgat gtactttaa ac

52

<210> SEQ ID NO 114
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 114

gtacctgtct tgtgtgaggc aacggcacct gtcttgttg aggcaacg

48

<210> SEQ ID NO 115
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 115

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tgtcttgtgt gaggcaacgg tctgtgtctt gtgtgaggca acggctcg 48

<210> SEQ ID NO 116
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 116

gtacctgtct tgtgtgaggc aacgggtacc tgtcttgtgt gaggcaacgg 50

<210> SEQ ID NO 117
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 117

tgtatatttg ttttgtgcct tctttctgtta attttgtttt gtgccttctt tc 52

<210> SEQ ID NO 118
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 118

gaaaagaaggc acaaaacaaa attacagaaa gaaggcacaa aacaaaattha ca 52

<210> SEQ ID NO 119
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 119

tacctgattt gtgtgaggca atggttacct gatttgttg aggcaatggt 50

<210> SEQ ID NO 120
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 120

tcatgttctg tgctctctct cgggatcatg ttctgtgctc tctctcggga 50

<210> SEQ ID NO 121
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 121

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cgttactcc ctttcggag gagaacgttg actcccttt cgaggagaa 50

<210> SEQ ID NO 122
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 122

gtttaattgt ggtctgccga tgtatggct taattgtggt ctgccatgt attt 54

<210> SEQ ID NO 123
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 123

gagtcggcta aacgaaggc ggggagtcgg ctaaacgaag gtccgg 46

<210> SEQ ID NO 124
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 124

gactccgggtt tttcttgc gttgctgact ccgggttttc tattgcgttg ct 52

<210> SEQ ID NO 125
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 125

ttggagaagg agcagaggtg aagttggaga aggagcagag gtgaag 46

<210> SEQ ID NO 126
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 126

ctccagagca cgctaccgag gtctccagag cacgctaccg aggt 44

<210> SEQ ID NO 127
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 127

ggactgatgt gcgcttgctg catgtggact gatgtgcgt tgtcgcatgt 50

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<210> SEQ ID NO 128
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 128

ttaaaccata ccataaggta tgatttaaa ccataccata agtactgatt 50

<210> SEQ ID NO 129
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 129

tcctccgtga gagtttgt gtgtctccgc tgagagtttg tgtgtg 46

<210> SEQ ID NO 130
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 130

ctctccgctg agagtttgt tttgtctcc gctgagagtt tgtgtgtg 48

<210> SEQ ID NO 131
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 131

gtgtgtttt gacgccctgt ttgcgtgt ctggacgccc ctgtttt 48

<210> SEQ ID NO 132
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 132

gtgtgtttt gacgccctgt tgctgttggt ggacgccctgt tt 42

<210> SEQ ID NO 133
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 133

gactgtttgc aatttattgt gagactgttt gcaatttattt gtga 44

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<210> SEQ ID NO 134
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 134

gaaagtttat ggaaaaatc tagaaagttt atggtttaa tcta

44

<210> SEQ ID NO 135
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 135

gatttagat ggcagaatgt gaggtggatt agagatggca gaatgtgagg tg

52

<210> SEQ ID NO 136
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 136

gctctgcgcg agtggcgac ttccgtgtc tgccgcgtg ggcgacttcg gt

52

<210> SEQ ID NO 137
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 137

cctgtttgt gtggggcaat ggtctgcctg tcttgtgtgg ggcaatggc tg

52

<210> SEQ ID NO 138
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 138

cctgtttgt gtggggcaat ggtctgtct tgtgtggggc aatggt

46

<210> SEQ ID NO 139
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 139

ggttgccgc aagtgttagtt aattcggtt ccgcgaatgt tagttatc

50

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<210> SEQ ID NO 140
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 140

agatggcaga tgtgagggtgt ctagatggca gatgtgagggt gtct

44

<210> SEQ ID NO 141
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 141

gtgtctgaga gaagtgtgac ctgtgtctga gagaagtgtg acct

44

<210> SEQ ID NO 142
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 142

agtggttatt gctcttggac gcagtggta ttgctcttgg acgc

44

<210> SEQ ID NO 143
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 143

aacgaatgt aatttatgtaa cgaacgaatg taattgtatgt aacg

44

<210> SEQ ID NO 144
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 144

ctggatctca gtgttatgtc tggctggatc tcagtgatgt gttgg

46

<210> SEQ ID NO 145
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 145

accgcttcta atagtcattt gacaccgtt ctaatagtcc attgac

46

<210> SEQ ID NO 146

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<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 146

gtaacgcata taatactaag tttgtaacgc atctataact aagttt

46

<210> SEQ ID NO 147
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 147

ccgtccaata cataaaatct taccgtccaa tacataaaat ctta

44

<210> SEQ ID NO 148
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 148

taatcagaat gtaatcgatg taaaacgtaat cagaatgtaa tcgatgtaaa cg

52

<210> SEQ ID NO 149
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 149

gttaaacgcata ctataaacta aggttaaacgc atctataaac taag

44

<210> SEQ ID NO 150
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 150

ggctttgtt ttggatttg aggtggctt tgttttggat ttggagggt

48

<210> SEQ ID NO 151
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 151

gtccctgttag actctgcttc agtccctgtta gactctgttt ca

42

<210> SEQ ID NO 152
<211> LENGTH: 42

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 152

ctagtgttgc tagtatgtgc actagtgttt ctagtatgtg ca

42

<210> SEQ ID NO 153
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 153

gtaatagatc tatgtggata cggtaataga tctatgtgga tacg

44

<210> SEQ ID NO 154
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 154

tgaaggcagag tctacaggga ctgaaacgaga gtctacaggg ac

42

<210> SEQ ID NO 155
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 155

cttctgtat agatctatgt ggatacgctt ctgtaataga tctatgtgga tacg

54

<210> SEQ ID NO 156
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 156

catgaatctc tcaaatacaa tgatttcatg aatctctcaa atacaatgtat tt

52

<210> SEQ ID NO 157
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 157

catgaatctc tcaaatacaa tgacatgaat ctctcaaata caatga

46

<210> SEQ ID NO 158
<211> LENGTH: 44
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 158

ccttctgtaa tagatctatg tgccttctgt aatagatcta tgtg

44

<210> SEQ ID NO 159
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 159

ttatacacac acaatagtca ttgttataca cacacaatag tcattg

46

<210> SEQ ID NO 160
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 160

cctgtgcacc ttttgtagta ttaccctgtg caccctttgt agtattac

48

<210> SEQ ID NO 161
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 161

caaatgtatt agctggggtt tatatagcaa atgtattagc tggggtttat atag

54

<210> SEQ ID NO 162
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 162

tggaagctgt tggcgcaagt cgatggaagc tgttggcgca agtcga

46

<210> SEQ ID NO 163
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 163

tattttgaat cattattattt tggactattt tgaatcatta ttatggac

50

<210> SEQ ID NO 164
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 164

cttggaaagg ttgtcgccca agtcttggaa gtttgcggc gcaagt 46

<210> SEQ ID NO 165
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 165

tgagtgtcat gaatctctca aatatgagtg tcatgaatct ctcaaata 48

<210> SEQ ID NO 166
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 166

atttggacctt ggaagtttgtt cggcattttgg acttggaaagt ttgtcgcc 48

<210> SEQ ID NO 167
 <211> LENGTH: 44
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 167

tttggaaagg ttgtcgccaa gtttggaaagt ttgtcgccgc aagt 44

<210> SEQ ID NO 168
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 168

tccaaaccctt gtgttatctct accatccaac ctttgttat ctctacca 48

<210> SEQ ID NO 169
 <211> LENGTH: 44
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 169

ccttgttat ctctaccatg ttcccttgtt atctctacca tgtt 44

<210> SEQ ID NO 170
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 170

acagcctcag cgcctccgg ggccacagcc tcagcgccct ccggggcc 48

<210> SEQ ID NO 171

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 171

aggaaaatca caactctgaa ttgagaaaa tcacaactct gaattt 46

<210> SEQ ID NO 172

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 172

atggggttct gtttataatc gtcatgggt tctgcttcta atcgta 46

<210> SEQ ID NO 173

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 173

ctctttgtgg tgccagacta tgcttttgt ggtgccagac tatgt 44

<210> SEQ ID NO 174

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 174

gtgataatata tctacgctgt ggttgtata attatctacg ctgtgggt 48

<210> SEQ ID NO 175

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 175

gctgcgaatt taactatggg gctgcgaatt taactatggg 40

<210> SEQ ID NO 176

<211> LENGTH: 42

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 176

ctacgctgtt ggtcttgtga actacgctgt tggctttgtg aa

42

<210> SEQ ID NO 177

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 177

ggtcttgtga agcactttat tgtggtcttg tgaagcactt tattgt

46

<210> SEQ ID NO 178

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 178

tttacgagggt tctgcttcta atcggttacga gggttctgctt ctaatc

46

<210> SEQ ID NO 179

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 179

tttcaatcgt cttttactgc ttcttaatcgt cttttactgc

40

<210> SEQ ID NO 180

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 180

ctgttgcttc ggccggacgtt ggctgttgct tcggccggacgtt atgg

44

<210> SEQ ID NO 181

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 181

gacgcccccg gaggttacaa accgacgccc ccggagggtt caaacc

46

<210> SEQ ID NO 182

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 182

ggacgcccggcc ggaggttaca ggacgcccggcc ggaggttaca

40

<210> SEQ ID NO 183
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 183

ccgccccggcg gtcggggccc ccaccgccccg gcgggtcgggg ccccca

46

<210> SEQ ID NO 184
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 184

caaccctcaa gccccggctt ggtcaaccct caagccccgg cttgggt

46

<210> SEQ ID NO 185
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 185

gcatctctga gcctaaaaga caagcatctc tgagcctaaa agacaa

46

<210> SEQ ID NO 186
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 186

gaaccctcgc tcggcccgta accgaaccct cgctcggccc gtcacc

46

<210> SEQ ID NO 187
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 187

gcctcggctt ggtgttgggg cgcctcggct tggtgttgggg gc

42

<210> SEQ ID NO 188
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 188
cacggccgccc ggaggttcaa aactcacgcc cgccggagggt tcaaaaact          48

<210> SEQ ID NO 189
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 189
cgccggagggt tcaaaaactct tattcgccgg aggttcaaaa ctcttatt          48

<210> SEQ ID NO 190
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 190
gtgctccagc cgctaaaccc ccaattcgtg ctccagccgc taaaccccca attc          54

<210> SEQ ID NO 191
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 191
cgccgccccga ggttcaaaaac ccggccgggg aggttcaaaa cc          42

<210> SEQ ID NO 192
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 192
ccggccggagg ttcaaaaccc tccggccggag gttcaaaaacc ct          42

<210> SEQ ID NO 193
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 193
aacgcgcacct cgctcggccgg caacgcgcgg tcgctcggcg gc          42

<210> SEQ ID NO 194
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
probe

<400> SEQUENCE: 194

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gctccgagcg cagtagcacg cgctccgagc gcagtagcac gc 42

<210> SEQ ID NO 195
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 195

ggttggcgcc ggtgccaga tgggttggcg ccggtgccca gatg 44

<210> SEQ ID NO 196
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 196

gtcgccgccc gaggttcgaa accgtcgccg ccggagggttc gaaacc 46

<210> SEQ ID NO 197
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 197

ccgccccggg ttcaaaaccc tccggggag gttcaaaacc ct 42

<210> SEQ ID NO 198
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 198

ttcgaaaccc tgaattctag tgttcgaaac cctgaattct agtg 44

<210> SEQ ID NO 199

<400> SEQUENCE: 199

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<210> SEQ ID NO 200
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 200

gagggtcgccg ccggagggttc gaagaggctg ccggccggagg ttcgaa 46

<210> SEQ ID NO 201

<211> LENGTH: 50

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 201

gcctggaggt cgccgcggc ggttcgccgt gaggtcgccc cccgagggttc 50

<210> SEQ ID NO 202
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 202

ccagatgggc ctggaggctc ccgcccagat gggcctggag gtcgccc 48

<210> SEQ ID NO 203
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 203

aagtacatcg gcggaccgc tgggaagtac atcggcggac ccgctggg 48

<210> SEQ ID NO 204
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 204

ggcggaccgc ctggggccct gagggcggac ccgctgggg cctgag 46

<210> SEQ ID NO 205
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 205

cgccctcgctc ggtggatccc cggaggcgcc tcgctcggtg gatccccggaa gg 52

<210> SEQ ID NO 206
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 206

ccggaggggca ttccagccgc taaaccggag ggcattccag ccgctaaa 48

<210> SEQ ID NO 207
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 207

ctggaaacag tgctgccacc ggtggactgg aaacagtgct gccacccggtg ga 52

<210> SEQ ID NO 208
 <211> LENGTH: 48
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 208

aagccggcca gacgacagcc ataaaagccg gccagacgac agccataaa 48

<210> SEQ ID NO 209
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 209

gccagacgac agccataaac cgccagacga cagccataaaa cc 42

<210> SEQ ID NO 210
 <211> LENGTH: 46
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 210

ctggaaacag tgctgccacc ggtctggaaa cagtgctgcc accggc 46

<210> SEQ ID NO 211
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 211

ggtggatggt gctgtctctc ggggtggatgg tgctgtctct cg 42

<210> SEQ ID NO 212
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 212

tggactacct aaactctgtt atggactacc taaaactctgt ta 42

<210> SEQ ID NO 213
 <211> LENGTH: 42
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 213

gtcaatctga atcaaactaa ggtcaatctg aatcaaacta ag

42

<210> SEQ ID NO 214

<211> LENGTH: 42

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 214

cggagtcggg tcgtgtctg acggagtcgg ttctgtctc ga

42

<210> SEQ ID NO 215

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 215

ctcgggtggg agtactctct ctcgctcggt ggtagtact ctctctcg

48

<210> SEQ ID NO 216

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 216

cggtggttag tgctctctc cggcggtgg tagtgctctc tctcg

46

<210> SEQ ID NO 217

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 217

tctctctcg gagggtgctg cctctctctc gggagggtgc tgcc

44

<210> SEQ ID NO 218

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 218

gttaattactt atctcgcttc ttgttaattac ttatctcgct tctt

44

<210> SEQ ID NO 219

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 219

cctttgggtg tccgagttgt attcccttgg gtgtccgagt tgtatt

46

<210> SEQ ID NO 220

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 220

tttcccgcgct ggactgtgta aatttcccgcg ctggactgtg taaa

44

<210> SEQ ID NO 221

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 221

cgcggttgtat gagactcagc ctcgcgttgt atgagactca gcct

44

<210> SEQ ID NO 222

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 222

ggcatacctt gggtgtccga gttgggcatac ctttgggtgt ccgagttg

48

<210> SEQ ID NO 223

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 223

taaagcaatt ggcagcctat atcttaaagc aattggcagc ctatatct

48

<210> SEQ ID NO 224

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 224

agcacaaaact gcatggcgaa agcacaaaact gcatggcgaa

40

<210> SEQ ID NO 225

<211> LENGTH: 42

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 225

cccattgaac ctatTTATTT tcccattgaa cctatTTATT TT

42

<210> SEQ ID NO 226
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 226

agcaattggc agcctatac tggagcaatt ggcagcctat atctgg

46

<210> SEQ ID NO 227
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 227

tcttaactgcc agttatatacg gcactcttac tgccagttat ataggcac

48

<210> SEQ ID NO 228
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 228

gtgtagaaca aactacgcag acgtgttagaa caaactacgc agac

44

<210> SEQ ID NO 229
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 229

ccaataagcc ttTTTtatcac ccaataagcc ttTTTtatcac

40

<210> SEQ ID NO 230
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 230

tctactccac tgcgttggaa ctcgtctact ccactgcgtt tggactcg

48

<210> SEQ ID NO 231
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<400> SEQUENCE: 231
agaacatagg ccccaagctg tagcagaaca taggccccaa gctgtacg 48

<210> SEQ ID NO 232
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 232
aaggcctctt ctattacctt tgtaaggcct cttctattac ctttgt 46

<210> SEQ ID NO 233
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 233
atcattacat tagaacatag gccatcattha cattagaaca taggcc 46

<210> SEQ ID NO 234
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 234
ggtgttttgt ccttcattt gcgggtgttt tgcctctcc attgcg 46

<210> SEQ ID NO 235
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 235
atatcaataa cacaaactaa caagatatac ataacacaaa ctaacaag 48

<210> SEQ ID NO 236
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 236
ctggcattttt ccgggtgtcc gagtctggca tcctccgggt gtccggat 48

<210> SEQ ID NO 237
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 237

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cttggtagtt tgtgttattt atatcttggtt agtttggtt attgatata 48

<210> SEQ ID NO 238
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 238

actcggacac ccggaggatg ccagactcggtt acacccggag gatgccag 48

<210> SEQ ID NO 239
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 239

ataaaaggag gtcatgacgg tataaaaggga ggtcatgacgt gt 42

<210> SEQ ID NO 240
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 240

ctaataaagg gagggtcatga cgctaataaa gggaggtcat gacgt 44

<210> SEQ ID NO 241
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 241

cgtcatgacc tccctttattt agcgtcatga cttcccttta tttag 44

<210> SEQ ID NO 242
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 242

accgtcatga cttcccttta taccgtcatgtt acctccctttt at 42

<210> SEQ ID NO 243
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 243

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<400> SEQ ID NO 244
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 244

cacggaaatt tccagagatg gattgcacgg aactttccag agatggattg 50

<210> SEQ ID NO 245
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 245

cacagtggtt gcaataccat gggtgacag tggttagcaat accatgggtg 50

<210> SEQ ID NO 246
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 246

cacagtggta gcaataccat gcacagtggt agcaatacca tg 42

<210> SEQ ID NO 247
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 247

gggcgttgg tctttggct ctgggcgtct tgtctttgg ctct 44

<210> SEQ ID NO 248
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 248

ggctctttgc ccaaagactc ggctcttgc ccaaagactc 40

<210> SEQ ID NO 249
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 249

cgccaggacc acaccataaa cctcgccagg accacaccat aaacct 46

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<210> SEQ ID NO 250
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 250

gccggccagga ccacaccata agccgcagg accacaccat aa

42

<210> SEQ ID NO 251
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 251

cgttacaaa ctgttgctc ggccgttacc aaactgttgc ctggc

46

<210> SEQ ID NO 252
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 252

caaccctcga accccctccgg gcaaccctcg aaccctcccg gg

42

<210> SEQ ID NO 253
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 253

gtattctggc gggcatgcct gtccgttattc tggcgggcat gcctgtcc

48

<210> SEQ ID NO 254
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 254

gatctgtatc cgcccccgac ccgatctgta tccggccccc accc

44

<210> SEQ ID NO 255
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 255

gtatccgccc ccgacccttc gatcgatcc gcccccgacc ctccgatc

48

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<210> SEQ ID NO 256
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 256

gagggttagcg ccgtttcatg gtcggagggt agcgccgtt catggtcg 48

<210> SEQ ID NO 257
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 257

ctaatctagg agtggcatacg aactaatcta ggagtggcat cgaa 44

<210> SEQ ID NO 258
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 258

cgcccatatc gagtttgcc tcggcgcca tatcgagttt tgcctegg 48

<210> SEQ ID NO 259
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 259

ttacaatgaa atcgactggt aatgcttaca atgaaatcga ctggtaatgc 50

<210> SEQ ID NO 260
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 260

acaatgaaat cgactggtaa tgcacaatga aatcgactgg taatgc 46

<210> SEQ ID NO 261
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 261

gcacacttgt cttgacttta ttgcacact tgtcttgact ttattc 46

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<210> SEQ ID NO 262
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 262

ggagcatgtc cacacttgc ttggaggatg tgcacacttg tcctt 44

<210> SEQ ID NO 263
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 263

cgagttgtga tggggcttgg atccgagttg tgatggggct tggatc 46

<210> SEQ ID NO 264
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 264

tccggatgtg aggaattgct gagttccgga tgtgaggaat tgctgagt 48

<210> SEQ ID NO 265
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 265

tacctctcct tcaagtacta tgttacctct cttcaagta ctatgt 46

<210> SEQ ID NO 266
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 266

attnaattctt caaccctct agctttatta aattctcaac ccctcttagct tt 52

<210> SEQ ID NO 267
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 267

aaattctcaa cccctcttagc ttaaattctc aaccctctta gctt 44

<210> SEQ ID NO 268

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<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 268

tggacttcat tttcatccac ctgtggactt cattttcata cacctg 46

<210> SEQ ID NO 269
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 269

tcttttcct gtagagtc atgttcttt tcctgtttaga gtctatgt 48

<210> SEQ ID NO 270
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 270

ttgttgttctt ttccaggat tttttcaggat attg 44

<210> SEQ ID NO 271
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 271

tttgtaaagg agagcttggaa ttgtgttgta aaggagagct tggattgt 48

<210> SEQ ID NO 272
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 272

tttgttattcc gagaggcatg cctgttgta ttccgagagg catgcctg 48

<210> SEQ ID NO 273
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 273

ttgcgcctct tggattcccg agagggttgcg cctcttgta ttccgagagg 50

<210> SEQ ID NO 274
<211> LENGTH: 44

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 274

catgttagtat gttgccagaa tgcatgttagt atggtgccag aatg

44

<210> SEQ ID NO 275
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 275

accatgttagt atggtgccag aatgaccatg tagtatgttg ccagaatg

48

<210> SEQ ID NO 276
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 276

tatcacaaac catgttagtat gtttatcaca aaccatgtag tatgtt

46

<210> SEQ ID NO 277
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 277

acatagaacg atctcatatt gaaacataga acgatctcat attgaa

46

<210> SEQ ID NO 278
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 278

actcttattg tatgttacat agaacactct tattgtatgt tacatagaac

50

<210> SEQ ID NO 279
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 279

agagtcatta aattctcaac cttagagtca ttaaattctc aacctt

46

<210> SEQ ID NO 280
<211> LENGTH: 48
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 280

caaggcttgg atgtgagagt tgctcaaggc ttggatgtga gagttgct 48

<210> SEQ ID NO 281
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 281

aaggggacggc ccggccgcagg aacccaaggg acggcccgcc gcaggaaccc 50

<210> SEQ ID NO 282
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 282

ctgcactccc caaatacatt ggcgctgcac tccccaaata cattggcg 48

<210> SEQ ID NO 283
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 283

gtgcactcc ccaaatacat tggcgctgca ctccccaat acattggc 48

<210> SEQ ID NO 284
<211> LENGTH: 46
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 284

ggactcgcgt taattcgcgt tccggactcg cgtaattcg cgttcc 46

<210> SEQ ID NO 285
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 285

cgcgttcctc aaattgattt gcggtcgcgt tcctcaaatt gattggcggt 50

<210> SEQ ID NO 286
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 286

tgttgcctcg gcggatcagc ccgctgttgc ctccggat cagccgc 48

<210> SEQ ID NO 287
 <211> LENGTH: 46
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 287

aaataaatca aaactttcaa caaaaataaa tcaaaaacttt caacaa 46

<210> SEQ ID NO 288
 <211> LENGTH: 46
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 288

cctcagcctg gagttccccc ggacctcagc ctggagttcc cccgga 46

<210> SEQ ID NO 289
 <211> LENGTH: 52
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 289

acattgagcc tgttgctggg gaagatacat tgaggctgt gctggggaa at 52

<210> SEQ ID NO 290
 <211> LENGTH: 44
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 290

ctcagectgg agttccccc gactcagcct ggagttcccc cgga 44

<210> SEQ ID NO 291
 <211> LENGTH: 52
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 291

catatcgagc ctgttgctgg ggaagacata tcgaggctgt tgctggggaa ga 52

<210> SEQ ID NO 292
 <211> LENGTH: 52
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 292

tatcgagct gttgctgggg aagacatatac gagcctgttg ctggggaga ca 52

<210> SEQ ID NO 293

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 293

agtccctcaac ctggggttcc gccgagtcct caacctgggg ttccggcg 48

<210> SEQ ID NO 294

<211> LENGTH: 52

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 294

agtccctcaac ctggggttcc gccggaagtc ctcaacctgg ggttccggcg ga 52

<210> SEQ ID NO 295

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 295

cgagtaagat ggaacatttt ggcgagtaag atggaacatt ttgg 44

<210> SEQ ID NO 296

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 296

tgc当地 accata gttctgccaa aattcgatac catagttc 48

<210> SEQ ID NO 297

<211> LENGTH: 50

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 297

gaatgccaaa attcgatacc atagtgaatg cccaaaattcg ataccatagt 50

<210> SEQ ID NO 298

<211> LENGTH: 50

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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probe

<400> SEQUENCE: 298

ctatccattt tgaaatcttg gtgcactatc cattttgaaa tcttgggtca 50

<210> SEQ ID NO 299

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<210> SEQ ID NO 300

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 300

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<210> SEQ ID NO 301

<211> LENGTH: 50

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<210> SEQ ID NO 302

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

<400> SEQUENCE: 302

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<210> SEQ ID NO 303

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<210> SEQ ID NO 304

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic probe

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<210> SEQ_ID NO 305
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<210> SEQ_ID NO 306
<211> LENGTH: 44
<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<210> SEQ_ID NO 307
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<210> SEQ_ID NO 308
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 308
atgtcaccac aaacagaaaac atgtcaccac aaacagaaaac                                40

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What is claimed is:

1. An array that comprises a first plurality of dimeric probes that hybridize to a first target nucleic acid sequence, wherein each of the dimeric probes comprise a first hybridizing nucleic acid sequence and a second hybridizing nucleic acid sequence linked together, wherein the first and second hybridizing nucleic acid sequences are the same and hybridize to the first target nucleic acid sequence, and wherein the first plurality of dimeric probes are selected from SEQ ID NO:4 to SEQ ID NO:9, SEQ ID NO:19 to SEQ ID NO:24, SEQ ID NO:28 to SEQ ID NO:33, SEQ ID NO:42 to SEQ ID NO:45, SEQ ID NO:48 to SEQ ID NO:51, SEQ ID NO:57, SEQ ID NO:58 and SEQ ID NO:73 to SEQ ID NO:301.

2. The array of claim 1, wherein the first and second hybridizing nucleic acid sequences are linked directly together.

3. The array of claim 1, wherein the first and second hybridizing nucleic acid sequences are linked together via a nucleic acid linker sequence.

50 4. The array of claim 3, wherein the nucleic acid linker sequence is a polyadenine linker.

5. The array of claim 1, wherein the dimeric probes are about 40-60 nucleotides in length.

55 6. The array of claim 5, wherein the dimeric probes are about 40-48 nucleotides in length.

7. The array of claim 5, wherein the dimeric probes are about 50-58 nucleotides in length.

60 8. The array of claim 1, wherein the array further comprises a second plurality of dimeric probes that hybridize to a second target nucleic acid sequence, wherein the second target nucleic acid sequence is from a fungal, viral, or bacterial pathogen.

65 9. The array of claim 8, wherein the first and second pluralities of dimeric probes hybridize to target nucleic acid sequences in the same pathogen.

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10. The array of claim 8, wherein the first and second pluralities of dimeric probes hybridize to target nucleic acid sequences in different pathogens.

11. The array of claim 8, wherein the array further comprises more than two pluralities of dimeric probes that hybridize to different target nucleic acid sequences. 5

12. The array of claim 11, wherein the more than two pluralities of dimeric probes hybridize to target nucleic acid sequences in the same pathogen.

13. The array of claim 11, wherein the more than two pluralities of dimeric probes hybridize to target nucleic acid sequences in different pathogens. 10

14. The array of claim 1, wherein the array further comprises pluralities of dimeric probes that specifically hybridize to target nucleic acid sequences in about 50 different pathogens. 15

15. The array of claim 1, wherein the array further comprises pluralities of dimeric probes that specifically hybridize to target Ob4Anucleic acid sequences in about 100 different pathogens. 20

16. The array of claim 1, wherein the first target nucleic acid sequence is from *Rhizoctonia solani*, *Pythium aphanidermatum*, *Fusarium solani* or *F. oxysporum*.

* * * *

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UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 9,222,125 B2
APPLICATION NO. : 13/448087
DATED : December 29, 2015
INVENTOR(S) : Ning Zhang

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the Claims

Claim 15, Line 19, please delete “target Ob4Anucleic acid sequences” and insert -- target nucleic acid sequences -- therefor.

Signed and Sealed this
Tenth Day of January, 2017



Michelle K. Lee
Director of the United States Patent and Trademark Office